

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 96572

TO: Gary Nickol

Location: cm-1/8d17/8e12

Art Unit: 1642

Friday, June 20, 2003

Case Serial Number: 513365

From: Mona Smith

Location: Biotech-Chem Library

CM1-6A01

Phone: 308-3278

mona.smith@uspto.gov

Search Notes

Thank you for using STIC services
Feel free to contact me if you have any questions.

Mona Smith 308-3278



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STIC-Biotech/ChemLib

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From: Sent:

Nickol, Gary Friday, June 13, 2003 3:56 PM STIC-Biotech/ChemLib

To:

Subject:

09/513365

Please search the following:

1) DNA of SEQ ID NO:2 2) DNA encoding the amino acids of SEQ ID NO:1

Thanks,

Gary Nickol CM1, AU:1642 Room 8D17, Mailbox 8E12 (703) 305-7143

Searcher: <u>M</u> .	Son. TH
Phone:	
Location:	
Date Picked Up:	61.6103
Date Completed:_	6120103
Searcher Prep/Rev	view: <u>4</u>
Clerical:	5
Online time:	5

TYPE OF SEARCH:
NA Sequences: 2
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:_

VENDOR/COST (where applic.) STN:_ DIALOG: Questel/Orbit:_ DRLink:_ Lexis/Nexis: Sequence Sys.:_ WWW/Internet:_ Other (specify):_

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-Q-/cgn2_1/USPTO_spool/US99513365/runat_16062003_124743_16453/app_query.fasta_1.455
-DB-EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0
-UNITS-blts -START-1 -END--1 -MATENIX-blosum62 -TRANS-human40.cd1 -LIST=45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM-ext -HEARSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US09513365_eCGNL_1_2874_erunat_16062003_124743_16453 -NCPU-6 -ICPU-3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPDEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                                                                                                              Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama, Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
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Meth. Enzymol. 303, 19-44 (1999)
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                                                                           HisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThr
                                                                                                                       CGGAG-CGGCTGCTCCTGCTACGTGCAGGACTAACTGGAGTGTGGAGTCGCTGCCC
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QPERSSRRPRRQRTSESRDLCHMTNGIDDCDDQPPKEKRSKSAKKKKRSKAKQEREAS
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/db_xref="GI:12849650"
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/translation="MQRNVSVLRELDNKYQETLKEIDDVYEKYKKEDDSNQKKRLQQH
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1 (bases 1 to 912)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
              found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM2058 row: h column: 10 High quality sequence stop: 587. Location/Qualifiers
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5', mRNA sequence.
BQ277444
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Tissue Procurement: NCI
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5'-AAGCAGTGGTATCAACGCGAGAGTGGCCATTACGGCCGGG-3' and 5' adaptors were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5'-ATTOTAGAGGCGGAGGGGGGGACATG-dri(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 1-2 kb size fraction (other fractions present in NHH_MGC_126 and NHH_MGC_128). Library created in the laboratory of T. Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC Library."
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/tissue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B (T1-phage-resistant)"
/note="Vector: pDNR-LIB; Site_1: Sfil (ggccattatggcc);
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Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
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                                                                                                                                   /Organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression for the see 'Creation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

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601587557F1 NIH_MGC_7
                                            Contact: Robert Strausberg, I
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                        NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, I
Unpublished (1999)
                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                            mRNA sequence
BE796780
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             cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
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Primates;
   Incyte
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   Genomics,
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   Inc.
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                  (LLNL)
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Best Local Similarity:
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High quality sequence stop: 769.
Location/Qualifiers
AAAGAAATCCAAGTCAGCAAAGAAAAAGAAACGCTCCAAGGCCAAGCAGGAAAGGGAAAGC
            uLysLysSerLysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAl 200
                                                                                                                                                    ArgAspLeu-CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGl
                                                                                                                AspSerSerGlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSer 160
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                                                CGTGATTTATTGTCACATGGCAAATGGGATTGAAGACTGTGATGATCAGCCACCTAAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/tcell_line="MGC3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
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21 SerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuProHis	1 MetLeuGlyGlnGlnGlnGlnGlnLeuTyrSerSerAlaAlaLeuLeuThrGlyGluArg 	3-365A-1 (1-280) x BI548536 (1-778)	Inent Scores: 6.31e-81	/db_xref="taxon:9606" /clone="IMAGE:526240" /clone=lib="MIH_MCC_95" /tissue_type="hippocampus" /lab_host="DHIOB" /note="Organ: brain; Vector: pBluescriptR (modified pBluescript Ks+); Site_1: BanHI; Site_2: Sal1-XhoI (gtcgag pBluescript Size 2:5 kb and normalized to ROT 5: This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NII_MGC Library." NT 237 a 176 c 227 g 138 t		# T D H	nih.gov Miklos Palkovits, M.D., Ph.D. ation: Michael J. Brownstein (NHGRI), Carninci (RIKEN) d by: The I.M.A.G.E. Consortium (LLNL) Incyte Genomics, Inc.	NIH-MGC Nationa Unpubli Contact	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 778)	BI548 BI548 EST. human	BI548536 778 bp mRNA linear EST 05- DN 603191255F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:526254	GTCTTG-GGGGAGATGATACGGTGT	220 lSerTyrGlyGluMetIleGlyCys 228	200 aSerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnVa
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                                                                                                                                                  University of Iowa
2024 University of Iowa
Tel: 319 356 4866
                                                                                                                                                                                     Contact: McCray, PB
McCray Lab
                                                                                                                                                                                                                                                                                       Eukaryota;
Mammalia; J
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                                   Genetics (www.resgen.com).
Seq primer: M13 FORWARD
                                                                                                                                                                                                                                        discovery
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                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                               Tissue
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                                                                                                                          Email: paul-mccray@uiowa.edu
                                                                       Pissue Procurement: Dr. M. J. Welsh, University of CDNA Library preparation: Dr. M. Bento Soares, University Arrayed by: Dr. M. Bento Soares, University DNA Sequencing by: Dr. M. Bento Soares, University
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M. Bento Soares, University c
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US-09-513-365A-1 (1-280) x BM982877
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TAG_TISSUE-Human Lung Epithelial Cell
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/db_xref="taxon:9606"
/clone="UI-CF-EN1-acs-d-05-0-UI"
/clone_lib="UI-CF-EN1"
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Qy 122 SerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMetAsp 141 	Qy 102 GlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGluLeuHis 121	Qy 82 LeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGluLysIle 101	Qy 62 GluileaspaspvaltyrGluLysTyrLysLysGluAspaspLeuAsnGlnLysLysArg 81	US-09-513-365A-1 (1-280) x BG184056 (1-798)	Best Local Similarity: 95.43% Mismatches: 10 Query Match: 67.96% Indels: 6 DB: 12 Gaps: 0	4.15e-76 Length: 1006.50 Matches:	130 g 293	indicated is HT1080, since sequence tags used, these sequence tags in HT1080 under normal circ	"See 'Creation of Genome-wide Protein Expression', les using Random Activation of Gene Expression', Biotechnology in press Note that even though	O (0 ··	rce	Email: 25 351 3530 Email: ScainGathersys.com High quality sequence stop: 531. FEATURES Location/Oualifiers	3201 Carnegie Ave, Cleveland, OH 44115, USA Tel: 216 431 9900 Fay: 716 341 0406	COMMENT Contact: Scott J. Cain Chart Athersys, Inc.	activation of gene expression AL Biotechnol. 19 (5), 440-445 (2001)	TITLE Creation of genome-wide protein expression libraries using random	AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith	_		ITION RST2972 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence SION BG184056	RESULT 7 BG184056/C LOCUS BG184056 798 bp mRNA linear EST 21-APR-2001	Qy 271 GluLysThrLysLysAspArgArgSerArg 280 	Db 255 GGGAAATGGTATTGCCCCAAAGTGCAGGGGAGATAATGAGAAAACAATGGACAAAAGTACT 196
/dev_stage="fetal and adult" /lab_host="DH10B (Life Technologies) (T1 phage resistant)"	/clone_lib="UI-E-EJI" /clone_lib="UI-E-EJI" /tissue_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and Chorold"	rce	searchers may obtain clc m). fiers	CDWA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa	2565 2565 36blue.weeg.uiowa.edu 2ment: Dr. Gregg Hageman	Program for Rat (University of Iov 451 Eckstein Medi	JOURNAL Genome Res. 6 (9), 791-806 (1996) MEDLINE 97044477 COMMENT Contact: Soares, MB	AUTHORS Bonaldo, M.F., L'ennon, G. and Soares, M.B. TITLE Normalization and subtraction: two approaches to facilitate gene	9 (EST. human. humon sapiens	ACCESSION BM719460 VERSION BM719460.1 GI:19038113	LOCUS BM719460 DEFINITION UI-E-EJ1-ajf-g-22-0-UI.rl UI-E-EJ1 Homo sapiens cDNA clone UI-E-EJ1-ajf-g-22-0-UI 5/ mRNA segmence	SOLT 8	Qy 262 ASTIGLUYSTITMETASDLYSSETTITG-ULLYSTITLYSTYSASDATGATGSETATG 280	264 TGTGTTTCACTTACCTATAAACCAAAGGGGAAATTGGTATTGCCCAAAGTGCAGGGGA	Qy 242 CysValSerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysGysArgGlyAsp 261	Qy 222 TyrGlyGluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSer 241	Qy 202 ProValGluPheAlaILeAspProAsnGluProThrTyrCysLeuCysAsnGlnValSer 221		182 LysSerLysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSer	Qy 162 AspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLys 181	Qy 142 SerSerGlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArg 161	Db 624 TCACAGTGTTTCCAAGATCCTGCTGAAAGTGAACGAGCCTCAGATAAAGCAAAGATGGAT 565

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       BI460319.1
                                                     mRNA sequence.
                                                                            603201967F1 NIH_MGC_97
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1 (bases 1 to 708)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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MetLeuGlyGlnGlnGlnGlnGlnLeuTyrSerSerAlaAlaLeuLeuThrGlyGluArg
                                                                                                                          ArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGluLys
                                                                                                                                                                                                                           LysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLysLys
                                                                                                                                                                                                                                                                                                                            AspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeu
                                                                                                                                                                                                                                                                                                                                                                                                    AGCCGGCTGCTCACCTGCTACGTGCAGGACTACCTTGAGTGCGTGGAGTCGCTGCCCCAC
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                                                                                                                                                                                                    AAGGAAATTGATGATGTCTACGAAAAATATAAGAAAGAAGATGATTTAAACCAGAAGAAA
                                                                                                                                                                                                                                                                                                     GACATGCAGAGGAACGTGTCTGTGCTGCGAGAGCTGGACAACAATATCAAGAAACGTTA
                                                                                                   CGTCTACAGCAGCTTCTCCAGAGAGCACTAATTAATAGTCAAGAATTGGGAGATGAAAAA
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a 163 c 213 g 122 t 1 others
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/db_xref="taxon:9606"
/clone="IMAGE:5267729"
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/lab_host="DH10B"
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Query Match: DB:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tissue Procurement: Dr. Gregg Hageman cDNA Library preparation: Dr. M. Bento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 discovery
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Bonaldo, M.F., Lenno
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Mammalia; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HisSerGinCysPheGinAspProAlaGluSerGluArgAlaSerAspLysAlaLys-Me
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       /dev_stage="fetal and adult"
//dev_stage="fetal and adult"
//lab_host="DH10B (Life Technologies) (T1 phage resistant)"
//note="Organ: eye; Vector: pT7T3-Pac (Pharmacla) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-EJ1 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               msoares@blue.weeg.uiowa.edu
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                                                                                                                                                                                                                                                          Choroid"
                                                                                                                                                                                                                                                                     /clone="UI-E-EJI-ajf-g-22-0-UI"
/clone_lib="UI-E-EJI"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
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/db_xref="taxon:9606"
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Eutheria; Primates; Catarrhini; Hominidae;
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          Eukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Primates; Ca
1 (bases 1 to 891)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
                                                                                                    BI091047.1
EST.
                                                                                                                             mRNA sequence
BI091047
                                                                            Homo sapiens
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602855235F1 NIH_MGC_10
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cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11022 row: e column: 10
High quality sequence stop: 722.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                      ArgargProArgargGlnArgThrSerGluSerArgAspLeuCysHisMetAlaAsnGly 169
AsnGluGlnCysProIleGluTrpPheHisPheSerCysValSerLeuThrTyrLysPro
                                               AsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGlyCysAsp
                                                                                              AAACGCTCCAAGGCCAAGCAGGAAAGGGAAGCTTCACCTGTTGAGTTTGCAATAGATCCT
                                                                                                            LysArgSerLysAlaLysGlnGluArgGluAlaSerProValGluPheAlaIleAspPro 209
                                                                                                                                                                             luSerGluArgAlaSerAspLysAlaLysMet-AspSerSerGlnProGluArgSerSer 149
                                                                                                                                                                                                                                                                                                                                                     GGTGGTTAATCGGCA-AGACATATGGAGTTACACTCACAGTGTTTCCAAGATCCTGTCTG
                                                                                                                                                                                                                                                                                                                                                                  uValGluAsnArgAlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspPro-AlaG 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGATGTTAAAACCCAGGAAGAGACGGTTCTACAGCCAGTCTTTCTCCCAGAGAGCACTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pAsp-LeuAsnGlnLysLysArg-------LeuGlnGlnLeuLeuGlnArgAla-Leu 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLys----GluAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5 kb. Library prepared by Life Technologies."

Technologies."

199 c 149 g 306 t
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/clone_lib="NIH_MGC_10"
/cell_line="MGC36"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -400P from Gibco
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BF114684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MetLeuGlyGlnGlnGlnGlnGlnLeuTyrSerSerAlaAlaLeuLeuThrGlyGluArg
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                                                                                                                                                                                                                                                                                                          libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHF pool 1:
105032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares Nb2HF8-9W pool 1:
758280-760583, 772104-774407 Soares NbHFA pool 1:
304776-305311, 320136-322823, 356280-32663 Soares NbHOT pool 1:
723720-726407, 739080-74099 Subtraction by Bento Soares and M. Fatima Bonaldo."
78 a 113 c 145 g 105 t
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a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:3391406"
/clone_1ib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
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FEATURES SOUICE	JOURNAL MEDLINE COMMENT	ORGANISM REFERENCE AUTHORS TITLE	RESULT 13 AV647917 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE	Qy	Qy Db	Db Qy	Db Db	0 Db
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 679) Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z. Hu,G., Gu,J., Chen,Z. and Han,Z. Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma	_	61 ArgAspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspGln 176	41 AspSerSerGlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSer	101 IleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGluLeu 120		14 ATGTTAGGGCAGCAGCAGCAACTGTACTCGTCGGCTGCCATCCTGACCGGGGAGCGG 73 21 SerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuProHis 40
CORGANISM HOMO Saplens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 564) AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,B.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J. TITLE Shotgun sequencing of the human transcriptome with ORF expressed	BE BE BE BE BE	141 AspSerSerGlnProGluArgS	Oy 101 IleGlnIleValThrGlnMetLeuGluLeuValGluAsnÅTgAlaArgGlnMetGluLeu 120 :::	81 ArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGluLys	61 LysGluileAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLysLys	Qy 21 SerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuProHis 40	17917 (1 LnGlnGln 	## Abse count

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                                                                                      MetLeuGlyG1nG1nG1nG1nLeuTyrSerSerAlaAlaLeuLeuThrG1yG1uArg
AspSerSerGlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSer 160
                                               HisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMet 140
                                                                                                                                                    AAGGAAATTGATGATGTCTACGAAAAATATAAGAAAGAAGATGATTTAAACCAGAAGAAA
                                                                                                                                                                                                                               LysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLysLys 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="FN0143"
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Seq primer: M13 Forward.
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/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C1
library is a subtracted library derived from the UI-R-C0
library, which is a subtracted library derived from the
UI-R-A1 and UI-R-E1 libraries. The UI-R-A1 library
consisted of a mixture of individually tagged normalized
libraries constructed from rat placenta, adult lung,
brain, liver, kidney, heart, spleen, ovary, and muscle.
The UI-R-E1 library consisted of a mixture of
individually tagged normalized libraries constructed from
8, 12 and 18-day embryo. The tag is a string of 3-5
nucleotides present between the Not I site and the
oligo-dT track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-C1) was constructed as follows: PCR
amplified cDNA inserts from UI-R-C0 clones from which 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Res. 6 (9),
                                      ESTs had been derived was used as a driver in a hybridization with the UI-R-CO library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C1 library. This procedure has been previously described and start of the control of
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-USER=US09513365_@CGN_1_1_396_@runat_16062003_124742_16434 -NCPU=6 -ICPU=3
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FH Key Location/Qualifiers FT CDS 1840 FT /*tag= a	Human; TSC403; INGIL; diagnosis; lung cance cell proliferation; cell aging; apoptosis; Homo sapiens.	Human ING1L enc	DT 18-OCT-1999 (first entry)	AX AC AAZ08595;	RESULT 1 AAZ08595 AAZ08595 standard; cDNA; 840 BP.	ALIGNMENTS	2 1807 22 2 1864 22	362 24.4 683 362 24.4 683	384.5 26.0 958 22	39 392.5 26.5 807 22	396.5 26.8 678 392.5 26.5 807	406 27.4 1465 22 400 27.0 699 21	427.5 28.9 1108 22 424.5 28.7 958 22	432.5 29.2 1365 24	446.5 30.1 1611 22	28 446.5 30.1 1465 21	447 30.2 1772 23 447 30.2 1781 21	466 31.5 693 24 455 30.7 1705 22	466 31.5 693 24	21 480 32.4 693 24	502 40.6 857	728 49.2 8487 22	728 49.2 2061 20 728 49.2 2886 24	728 49.2 2061 18	728 49.2 1902 19	728 49.2 1143 22 AAH2847 728 49.2 1902 18 AAT6965	50.3 1835 21 AAA5378	853.5 57.6 1533	853.5 57.6 911 21 AAA537.9	1345 90.8 1153 21 AAZ4 874.5 59.0 2817 21 AAA5	1 100.0 1080 22 AAD1278	1481 100.0 840
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03-FEB-1998;
05-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 14; Page 91; 99pp;
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                                            SerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnVal
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US-09-513-365A-1 (1-280)
                                                         Score:
                                                                  Alignment Pred. No.:
                                                                                                            The present sequence is a DNA encoding tumour suppressor homologue protein, p33ING2 which is homologous to human tumour suppressor prop47ING3. The tumour suppressors of the invention are involved in the regulation of cell proliferation and in the control of cellular agi anchorage dependence and apoptosis. The tumour suppressor protein, p47ING3, nucleic acids encoding it and antibodies against it are us for diagnosis, prevention and treatment of tumours and cancers. The p47ING3 DNA is also used in gene therapy.
                                                                                           Sequence 1080
                                                                                                                                                                                                                       New tumor suppressor tumors -
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                                                               Location/Qualifiers
277..999
                /product= TUSUP
/note= "Tumour s
                                                                                                                                              protein; TUSUP; human; car
t; gastrointestinal tract;
                                                                                                                                                                                                                                                                                               cDNA;
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P-PSDB;
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                                                                 CCGTCGCGGATCCTGGCTCCGCAAACGTTAAAGGAAATTGATGATGTCTACGAAAAATAT
                                                                                                                               CGGTGATGTTTCCAACCTCTTTCCCAGTCAATGGATCAGGACGGCGATCAGCAGCTCGGA
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Zeremski M,
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CC remains unknown but p53 has been found to act in cooperation with CC ING1. Functional cooperation between ING1 and p53 suggested that CC ING1 encoded a tumour suppressor protein that functioned within the CC ING1 encoded a tumour suppressor protein that functioned within the CC Expanding of the ingline and chromosomal location of the ING1 placed it CC within a region that is frequently rearranged in head and neck cancers and chromosomal location of the ING1 placed it CC expression suggesting that ING1 was not a useful gene to study in CC expression suggesting that ING1 was not a useful gene to study in CC expression of one promoter (la) produces a protein identical to CC Expression of a second promoter (la) produces a protein having CC expression of a second promoter (lb) produces a protein having CC expression of a second promoter (lb) produces a protein having CC expression of a second promoter (lb) produces a protein having CC expression of a second promoter (lb) produces a protein having CC expression of a second promoter (lb) produces a protein having CC expression of a second promoter (lb) produces a protein having CC expression of a second promoter (lb) produces a protein having CC expression of a second promoter (lb) produces a protein having CC expression of a second promoter (lb) produces a protein having CC expression of a second promoter (lb) produces a protein having CC expression of a second promoter (lb) produces a protein having CC expression of a second promoter (lb) produces a protein having CC expression of a second promoter (lb) produces a protein having CC expression of a second promoter (lb) produces a protein having cancers in the sequence of expressing the conclusion of the sequence of expressing the conclusion of the sequence of expressing the conclusion of the sequence of the polymental produces and the conclusion and the conclusion and the conclusion of the sequence of the polyment of ccll conclusions and the conclusion and the conclusion and the conclusion and the conclusion and c
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Sequence 2817
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Alignment Scores: 7.04e-74 Length: 2817 Score: 874.50 Matches: 165 Percent Similarity: 77.41% Conservative: 44 Pest Local Similarity: 61.11% Mismatches: 50 Query Match: 59.05% Indels: 15 DB: Gaps: 3

US-09-513-365A-1 (1-280) x AAA53790 (1-2817)

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     Detecting nucleic acid encoding exon 1b of ing1, useful for diagnosing and treating cancer, comprises contacting sample with isolated nucleic acid comprising sequence of exon 1b and detecting hybridized products
                                                                                                                                                                                                                     p53; tumour; cancer; detection; antibody; hybridisation; exon 1b; ING1; ing1; p33ING1; p37ING1; oncogene; gene therapy; diagnosis; proliferation disorder; transformation; transformed cell; human; ds
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CC p53 pathway. This data suggested a possible role for ING1 head and neck cancers and chromosomal location of the ING1 placed it CC within a region that is frequently rearranged in head and neck cancers. Large scale analysis of tumours involving ING1 has not CC revealed mutations in ING1 nor significant variations in its CC expression suggesting that ING1 was not a useful gene to study in CC expression of one promoter (la) produces a protein identical to CC Expression of one promoter (la) produces a protein identical to CC Expression of a second promoter (1b) produces a protein having the involving ING1 has been CC ING1. Expression of a second promoter (1b) produces a protein having CC ING1. Expression of a second promoter (1b) produces a protein having CC ING1 Expression of a second promoter (1b) produces a protein having CC ING1 Expression of a second promoter (1b) produces a protein having CC ING1 matched p37ING1 (Wild type: p33ING1). p37ING1 has the CC ING1 Expressing wild type: p33ING1). p37ING1 has the CC ING2 expressing wild type: p33ING1). p37ING1 is able to cause CC ING2 expressing the sequence of exon 1b of ing1 by hybridisation with an CC isolated nucleic acid having the sequence of exon 1b of ing1 can also be used to raise antibodies that can also be used to raise antibodies CC ING2 expressing the useful in gene therapy for treatment of cell concipied of p37ING1 can also be used to raise antibodies contained and isorders, especially cancers and for diagnosing and certained contained and certained concipied and solutions, especially cancers and for diagnosing and certained contained to cancers and contained concipied contained contained to cancers and contained cont
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Sequence 911 BP; 228 A; 255 C; 305 G; 123 T; 0 other;

	(1-911)) x AAA53792	US-09-513-365A-1 (1-280) x AAA53792 (1-911)
ω	Gaps:	21	DB:
15	Indels:	57.63%	Query Match:
51	Mismatches:	59.19%	Best Local Similarity:
45	Conservative:	75.74%	Percent Similarity:
161 .	Matches:	853.50	Score:
911	Length:	1.65e-72	Pred. No.:
			Alignment Scores:

145	131SerGluArgAlaSerAspLysAlaLysMetAspSerSerGlnPro 145	2γ 1
419	360 GTGGACAGCCACGTGGAGCTGTTCGAGGCGCGCAGCAGGAGCTGGGCGACACAGTGGGCAAC 419	Db 3
130	lsSerGlnCysPheGlnAspProAlaGlu	2γ 1
359	300 GACGAGAAGATCCAGATCGTGAGCCAGATGGTGGAGCTGGTGGAGAACCGCACGCGGCAG 359	Db 3
117		Ωy
299		200
97	78 GlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGly 97	Ωy
239	180 GAGATCCTGAAGGAGCTAGACGAGTGCTACGAGCGCTTCAGTCGCGAGACAGAÇGGGGCG 239	Db 1
77	58 GluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsn 77	Ωy
179	120 CTGCCTTTCGACTTGCAGAGAAATGTCTCGCTGATGCGGGAGATCGACGCGAAATACCAA 179	Db 1
57	38 LeuProHisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGln	Дy
119	63 GGGAGCACCTCCACCTGGTGAACTATGTGGAGGACTACCTGGACTCCATCGAGTCC 119	
37	rArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSer	Дy

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes a human cancer associated antigen. The sequence is a variant of the ING1 gene, which is a tumour The sequence is a variant of the ING1 gene, which is a tumour suppressor gene candidate. The cancer associated antigen polynucleotides and polypeptides are useful for screening for the possible presence of a pathological condition in a subject such as cancer. The cancer associated antigen polypeptides are useful for producing vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
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                                                                                    GluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsn
                       CysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysValSerLeuThrTyr
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  AAGAAGAAGCGCTCCAAGGCCAAGGCGAGCGAGAGGCGTCCCCTGCCGACCTCCCCATC
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cc combination, to specifically recognise epitopes of ING1 (inhibitor of CC growth 1) protein isoforms. ING1 is a tumour suppressor gene and its CC expression is regulated through the cell cycle, peaking in the S phase. CC malignancies. Overexpression of a construct containing the ING1 gene is CC able to inhibit cell growth by reducing the fraction of cells which enter CC into the S phase. The monoclonal antibodies are useful for detecting an CC ING1 protein in a cell, which involves selecting a cell that ectopically CC or endogenously expresses ING1 protein. The anti-ING1 monoclonal antibody consists of two or more antibodies of CAb1-CAb10 (not consists of two or more antibodies are also useful for diagnosing a disease e.g. tumour or medical condition in an animal C (preferably, human) associated with aberrant levels of an ING1 protein.
             RESULT 8
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p33ING1b.
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suppressor; cell cycle; l
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breast tumour; lymphoid malignancy;
; diagnosis; tumour; antigen;
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                                                                     GACCCCAACGAACCCACGTACTGTCTGTGCAACCAGGTCTCCTATGGGGAGATGATCGGC
                                                                                                                AspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMetILeGly
                                                                                                                                                    LysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProValGluPheAlaIle
                                                                                                                                                                                        AsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSerLysSerAlaLys
                                                                                                                                                                                                                            GTGGACAGCCACGTGGAGCTGTTCGAGGCGCAGCAGGAGCTGGGCGACACAGCGGGCAAC
                                                                                                                                                                                                                                                                                                                                                                              GlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                GluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsn
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AAAGCCCTGGAGAAATCCAAAAAAGAGAGG
           LysSerThrGluLysThrLysLysAspArg
                                                                                                                                            AAGAAGAAGCGCTCCAAGGCCAAGGCGGAGCGAGAGGCGTCCCCTGCCGACCTCCCCATC
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RESULT

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Alignment Scores: Pred. No.: Score:
                                                                                                                  CC the p53 pathway occurs in a much larger proportion of tumours. In cc many cases the mechanism of functional inactivation of the p53 gene CC remains unknown but p53 has been found to act in cooperation with CC ING1 Functional cooperation between ING1 and p53 suggested that CC ING1 encoded a tumour suppressor protein that functioned within the CC p53 pathway. This data suggested a possible role for ING1 in head CC and neck cancers and chromosomal location of the ING1 placed it CC within a region that is frequently rearranged in head and neck cancers. Large scale analysis of tumours involving ING1 has not revealed mutations in ING1 nor significant variations in its cancer etiology. However, alternative initiation exons of the ing1 CC cancer etiology. However, alternative initiation exons of the ing1 CC cancer etiology. However, alternative initiation exons of the ing1 CC cancer etiology. However, alternative initiation exons of the ing1 CC cancer etiology. However, alternative initiation exons of the ing1 CC cancer etiology. However, alternative initiation exons of the ing1 CC cancer etiology. However, alternative initiation exons of the ing1 CC cancer etiology. However, alternative initiation exons of the ing1 CC cancer etiology. However, alternative initiation exons of the ing1 CC cancer etiology. However, alternative (lb) produces a protein having CC cancer etiology. However, alternative (lb) produces a protein having CC cancer etiology. However, alternative (lb) produces a protein having CC cancer etiology. However, alternative (lb) produces a protein having CC cancer etiology. However, alternative (lb) produces a protein having CC cancer etiology. However, alternative (lb) produces a protein having CC cancer p37ING1 (wild type p33ING1). p37ING1 has the collection of transformation of those cells. Thus detecting a concern part of the p37ING1 to a sale to the part of the part of the ing1 cancers.

CC concern to a second protein having the sequence of exon lb of ing1 the collection with an ing1 cancer part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting nucleic acid encoding exon 1b of ing1, useful for diagnosing and treating cancer, comprises contacting sample with isolated nucleic acid comprising sequence of exon 1b and detecting hybridized products
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                                                                         Sequence 1835 BP; 541 A; 387
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                                                                                                                                                              sequence of a human cancer associated
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                                   Location/Qualifiers 16..900
/transl_except= "(pos: 25..30,
                                                                                                                            antigen; ING1; tumour suppressor; cancer; vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated cancer associated nucleic acid molecule identified by SEREX (serological identification of antigens by recombinant expression cloning) technique, useful in nucleic acid based therapies to treat cancer -
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                                                                                   {\tt GlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeu}
                                                                                                                       GGCAACAGCGGCAAGGTTGGCGCGGACAGGCCCAATGGCGATGCGGTAGCGCAGTCTGAC
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          A partial cDNA clone (AAT69651), designated ING1, codes for a tumour suppressor protein p33ING1 (AAW19118) that is a potent inhibitor of cell growth. It was isolated by subtractive hybridisation between normal mammary and transformed epithelia cDNAs, isolation of an antisense ING1 cDNA insert that caused increased cell proliferation, and use of the insert to screen normal human fibroblast and HeLa cDNA libraries. A complete I sequence (AAT69652) was obtd. by 5'RACE. ING1 is localised to 13933-34 chromosome region, to which a number of human cancers been marked.
                                                                                                                                                                                                                   Isolated tumour suppressor gene, ifor inhibiting or increasing cell treatment or diagnosis of cancer
                                                                                                                                                                                     Claim 1; Fig 2; 63pp;
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08-DEC-1995;
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epithelial

LysThrMetAspLysSerThrGluLysThrLysLysAspArg SerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu GluMetI1eGlyCysAspAsnGluGlnCysProI1eGluTrpPheHisPheSerCysVa1 GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly LysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal AAGACCTCCAAGAAGAAGAAGCGCTCCAAGGCCAAGGCGGAGCGAGAGGCGTCCCCTGCC partial cDNA. p33ING1; breast ING1 - useful to proliferation, i cancer; in particular for 885 277 brain cancer; novel 843 263 243 723 223 663 783

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RESULT 12
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Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores: Pred. No.: Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             breast cancer; a decreased level cells. They can also be used in proliferation of cancer cells.
Partial ING1 partial cDNA sequence.
                       18-JAN-1999
                                            AAV62285
                                                               AAV62285 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1902 BP;
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                                                                                                          AAGACCATGGACAAAGCCCCTGGAGAAATCCAAAAAAAGAGAGG
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US-09-513-365A-1 (1-280) x AAV62285 (1-1902)
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Query Match:
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                                                                                                                                                                                                                     Alignment Scores
                                                                                                                                                                                                                                                                                                                                               CC performed with cDNA from normal mammary epithelial cells, and CC subtracted cDNAs were cloned into retrovirus vector pLNCX. Following passage through a packaging line, normal mouse mammary completed cells were injected, and infected cells were injected cells were injected cells were injected cells were injected completed into nude mice. Putative transforming fragments from tumours were completed into nude mice. Putative transforming fragments from tumours were completed by PCR (see AAV62290-91) and subcloned into LNCX. An ING1 cragment was obtained and used to screen normal human fibroblast cell cDNA libraries. 2 Clones were sequenced to obtain cell partial ING1 sequence. The complete cDNA sequence (see CAV62292) was obtained by RACE. A claimed method to potentiate capoptosis in a eukaryotic cell involves administering an active complete encoding such as a peptide. CC alaimed method for inhibiting apoptosis in a eukaryotic cell completed. Also claimed completed and method for determining the apoptotic characteristics of a cell are a method for determining the apoptotic characteristics of a cell substantially free of p33ING1 biological activity. The invention cold sections in Inderivatives or variants that may be used to induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the nucleotide sequence of a human ING1 (INhibitor of Growth) partial cDNA clone that codes for a pl33ING1 polypeptide (see AAW79574), a novel inhibitor of cell growth land a candidate tumour suppressor. ING1 is a new gene that is expressed in normal mammary epithelial cells, but which is expressed only at lower levels in several cancerous mammary epithelial cell lines and is not expressed in many primary brain tumours. To isolate ING1, a subtractive hybridisation of breast cancer cell lines cDNAs was subtractive hybridisation of breast cancer cell line cDNAs was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modulating eukaryotic apoptosis by increasing p33ING1 activity using p33ING1 derivatives, to induce apoptosis in cancer cells, in the investigation of apoptotic pathways
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brain tumour; gene therapy; tumour suppressor; ss
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2C A full-length cDNA clone (AAT69652), designated ING1, codes for a covel 33 kDa tumour suppressor protein p33ING1 (AAW19119), formerly p33ING1, that is a potent inhibitor of cell growth. A partial clone (AAT69651) was isolated by subtractive hybridisation between normal mammary and transformed epithelial cDNAs, isolation of an antisense ING1 cDNA insert that caused increased cell proliferation, and use of the insert to screen normal human fibroblast and HeLa cDNA libraries. The complete ING1 sequence was then obtd. by 5'RACE. ING1 is localised to the 13q33-34 chromosome region, to which a number of human cancers have been mapped. ING1 nucleic acids can be used in the diagnosis of breast cancer; a decreased level of ING1 mRNA indicates cancerous cells. They can also be used in gene therapy methods to block the proliferation of cancer cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated tumour suppressor gene, ING1 - useful to develop products for inhibiting or increasing cell proliferation, in particular for treatment or diagnosis of cancer
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P-PSDB; AAW18119.
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                                                                                         CGGCAGGTGGACAGCCACGTGGAGCTGTTCGAGGCGCAGCAGGAGCTGGGCGACACAGTG
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  This is the nucleotide sequence of a human ING1 (INhibitor of Growth) that codes for a pl331NG1 polypeptide (see AAW79675), a novel inhibitor of cell growth and a candidate tumour suppressor. ING1 is a new gene that is expressed in normal mammary epithelial cells, but which is expressed only at lower levels in several cancerous
                                                                                                      Modulating eukaryotic apoptosis by increasing p33ING1 using p33ING1 derivatives, to induce apoptosis in cand in the investigation of apoptotic pathways
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
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                                                                                Claim
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)B; AAW79675.
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                                                                               3; 66pp; English.
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ppressor; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC mammary epithelial cell lines and is not expressed in many primary CC brain tumours. To isolate ING1, a subtractive hybridisation of CC breast cancer cell line cDNAs was performed with cDNA from normal CC mammary epithelial cells, and subtracted cDNAs were cloned into CC retrovirus vector pLNCX. Following passage through a packaging CC line, normal mouse mammary epithelial cells were infected, and CC infected cells were injected into nude mice. Purative transforming CC fragments from tumours were isolated by PCR (see AAV62290-91) and CC screen normal human fibroblast and HeLa cell cDNA libraries. 2 CC clones were sequenced to obtain a partial ING1 sequence (see CAAV62285). The complete cDNA sequence was then obtained by RACE. A CC claimed method to potentiate apoptosis in a eukaryotic cell involves administering an active p33ING1 peptide or an CC inhibiting apoptosis in a eukaryotic sell involves administering an active p33ING1 activity in a eukaryotic cell, and an isolated eukaryotic characteristics of a eukaryotic cell, and cassay for determining the level of p33ING1 activity in a eukaryotic cell substantially free of p33ING1 activity. The invention discloses ING1 derivatives or call and an isolated eukaryotic cell substantially free of p33ING1 activities or ariants that may be used to induce apoptosis in eukaryotic cancer
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{\tt GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysValue}
                           GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly
                                                                                             LysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal
                                                                                                                                                                                                                                                                                                                    ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu----
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                                                                                                                                                                                     GGCAACAGCGGCAAGGTTGGCGCGGACAGGCCCAATGGCGATGCGGTAGCGCAGTCTGAC
                                                                               AAGACCTCCAAGAAGAAGAAGCGCTCCAAGGCCAAGGCGGAGCGAGAGGCGTCCCCTGCC
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                                                                                           This is the nucleotide sequence encoding the human p33-ING1 protein, cused in the method of the invention. The ING1 gene encodes p33-ING1 which can be used to modulate the activity of, isolate or detect p53. Expression of the ING1 and p53 genes in a mammalian cell results in normal growth regulation anchorage-dependent growth and apoptosis as a response to irreversible DNA damage and other cellular insult. Inhibition of expression of either gene results in a loss of cellular growth control, anchorage independent growth, inhibition of apoptosis and resistance to radiation and cytotoxic drugs. The p33-ING1 is a component of the p53 signalling pathway that cooperates with p53 in negative regulation of cell proliferation by modulating p53 dependent transcriptional activation. Biological function of p53 signalling pathway can therefore be regulated (both enhanced or suppressed) by modulating p33-ING1 activity. The modulation of p33-ING1 activity can
                                              be used for the stimulation or restoration of the p53 pathway in anti cancer therapy or for the suppression of the p53 pathway to defend sensitive tissues from genotoxic stress or for the general
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-263685/22
P-PSDB; AAY03244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; p33-ING1 protein; growth regulation; apoptosis; DNA damage; inhibition; anchorage independent growth; cytotoxic drug; transcriptional activation; cancer; immortal cell line; ss.
                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 1; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                      Use of p33-ING1 peptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-APR-1999
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26-SEP-1997;
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                                    immortal cell lines.
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AAGACCATGGACAAAGCCCTGGAGAAATCCAAAAAAGAGAGG 885
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97US-0060138.
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/product= "human p33-ING1 protein"
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Db 84	Ωу 26	Db 78	ОУ 24	Db 72	Оу 22	Db 66	Оу 20	Db · 60	Оу 18	Db 54	Qy 16	Db 49	Qу 14	Db 43	Qу 13	Db 37	Qy 116	Db 31	Q у 9	Db 25	Qу 7	Db 19	ΩУ 5	us-09-513-36	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarit Query Match: DB:
4	04 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277	34 GGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCAAGTGCCGGGGGGAGAACGAG 843	4 S	24 GAGATGATCGCCTGCGACAACGACGAGTGCCCCCATCGAGTGGTTCCACTTCTCGTGCGTG	4	GACCTCCCCATCGACCCCAACGAACCCACGTACTGTCTGT	04 GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly 223)4 AAGACCTCCAAGAAGAAGAAGCGCTCCAAGGCGGAAGGCGGAGCGAGAGGCGTCCCCTGCC 663	4.	44 GCGTCCAGCAACCACGACGACGACGACGCGCGTCGGGCACACCCAAGGAAGAAGAAGGCC 603	4	0 A	4	30 GGCAACAGCGGCAAGGTTGGCGGGGCAGAGGCCCAATGGCGATGCGGTAGCGCAGTCTGAC 489	.31SerGluArgAlaSerAspLysAlaLysMetAspSerSer 143			O CTGGGCGACGAGAAGATCCAGATCGTGAGCCAGATGGTGGAGCTGGAGAACCGCACG 369	ō	O GGGCGCAGAAGCGGCGGATGCTGCACTGTGTGCAGCGCGCGC	σ	0	56 TyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAsp 75	55A-1 (1-280) x AAX28688 (1-2061)	Scores: 5.14e-60 Length: 2061 728.00 Matches: 136 milarity: 74.79% Conservative: 39 Similarity: 58.12% Mismatches: 45 h: 49.16% Indels: 14 20 Gaps: 2

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Search completed: June 20, Job time: 250 secs 2003, 02:49:55

Sequence 2061 BP;

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1080)
Harris, C. C. and Nagashima, M.
Tumour suppressor gene, p4/1093
Patent: WO 0159114-A 7 16-A0G-2001;
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
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/organism="Homo sapiens"
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                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Shimada,Y., Saito,A. and Horle,M.
Shimada,Y., Saito,A. and Horle,M.
Subricts (bubission
Submitted (07-APR-1998) Yoshikazu Shimada, Otsuka Pharmaceutical
Co. Ltd., Otsuka GEN Research Institute; Kagasuno, Kawauchi-cho,
Tokushima, Tokushima 771-0192, Japan
(E-mail:shim@ctsuka.genome.ad.jp, Tel:81-886-65-2888(ex.2476),
Fax:81-886-37-1035)
                                                                                                                                   1 (sites)
Shimada,Y., Saito,A., Suzuki,M., Takahashi,E. and Horie,M.
Cloning of a novel gene (INGIL) homologous to ING1, a candidate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeu
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                                                                      Homo sapiens fetal tissue_lib:fetal-brain cDNA to mRNA.
Homo sapiens
Homo sapiens ING1L mRNA for ING1Lp, complete cds. AB012853
AB012853.1 GI:4115554
                                                                                                                                                                            tumor suppressor
Cytogenet. Cell Genet. 83 (3-4), 232-235 (1998)
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Conservative:
Mismatches:
Indels:
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1. .1078
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Location/Qualifiers
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92. .934
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1080)
Nagashima, M., Shiseki, M., Miura, K., Hagiwara, K., Linke, S.P.,
                                                                                                                                                        SerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuProHis
                                                                      AspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeu
                                                                                                   IleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGluLeu
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                                                                                                                                                                                                                                AspSerSerGinProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSer
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                              MetLeuGlyGlnGlnGlnGlnLeuTyrSerSerAlaAlaLeuLeuThrGlyGluArg
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Homo sapiens p33 (ING2) mRNA, complete cds.
AF053537
  Gaps:
               US-09-513-365A-1 (1-280) x AX211560 (1-1080)
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Shiseki, M., Miura, K., Hagiwara, K., Linke, S.P.,

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NVSVIRELDNKYQETLKEIDDVYEKYKKEDDLNQKKRLQQLLQRALINSQELGDEKIQ
IVTQMLELVENRARQMELHSQCFQDPAESBRASDKAKMDSSQPERSSRRPRRQRTSES
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QVSYGEMIGCDNEQCPIEWFHFSCVSLTYKPKGKWYCPKCGBDNEKTMDKSTEKTKKD
RRSR"
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redeux,R., Wang,X.W., Yokota,J., Riabowol,K. and Harris,C.C. DNA damage-inducible gene p331NG2 negatively regulates cell proliferation through acetylation of p53 proc. Natl. Acad. Sci. U.S.A. 98 (17), 9671-9676 (2001) 21396501
                                                                                                                                                                  Carcinogenesis,
Bldg.37 Rm.2C01,
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Conservative:
Mismatches:
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a 196 c 271 g
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RDLCHAANGTBDCDQPPREKKSKSAKKKRSKAKQBREASPYEFAIDPNBPTYCLCN
QVSYGEMIGCDNEQCPIEWFHFSCVSLIYKPKGKWYCPKCRGDNEKTMDKSTEKTKKD
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Series: IRAL Plate: 15 Row: m Column: 11
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA g1: 4504694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 ArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGluLys
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                                                                  // 1141/
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/db_xref="LocusID:3622"
/db_xref="taxon:9606"
/clone="MGC:10524 IMAGE:3941655"
/tissue_type="Lung, small cell card
/clone_lib="NHL MGC_7"
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Matches:
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Email: cgapbs.mity usan
Lissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Prayed by: The I.M.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gailthersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@ehgri.nih.gov
Contact: nisc_mgc@ehgri.nih.gov
Akhter.N., Ayele.R., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guna,X., Gupta,J., Haghighi,P.,
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Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J.,
Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C.,
Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A.,
Zhang,L.-H. and Green,E.D.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1141)
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National Cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (07-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                  HisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMet
                                                                                                                                                                                                                                    BC030128 1141 bp mRNA linear PRI 20-MAY-Homo sapiens, inhibitor of growth family, member 1-like, clone MGC:10524 IMAGE:3941655, mRNA, complete cds.
                                                                    AspSerSerGlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSer
                                                                                       LysLysSerLysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAla
                                                                                                                                                                                                                                                                                                                                                       SerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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KEYWORDS
SOURCE
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WetLeuGlyGlnGlnGlnGlnLeuTyrSerSerAlaAlaLeuLeuThrGlyGluArg 20	Qy 61 LysGlulleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLysLys 80	OY 101 IleGinileValThrGinMetLeuGluLeuValGluAsnArgAlaArgGinMetGluLeu 120		Oy 181 LysLysSertJashalLysLysLysLysLysAgerLyslathysGluAla 200	Qy 221 SerTyrGlyGluWetileGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPhe 240	261 AspasnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArgArgSerArg 	LOCUS AFVINESS TO US 33 ING2 (Ing2) MRNA, complete cds. ACCESSION AF078834 VERSION AF078834.1 GI:10039542	NETWORDS NORGE WAS MUSCULUS. ORGANISM MUS musculus. ORGANISM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. REFERENCE 1 (bases 1 to 1001) AUTHORS Nagashima,M., Hagiwara,K., Hancock,A.R. and Harris,C.C. TITLE Direct Submission JOURNAL Submitted (16-JUL-1998) Laboratory of Human Carcinogenesis, National Cancer Institute, National Institutes of Health, 37 Convent Dr., Bldg. 37, Rm. 2C01, Bethesda, MD 20892, USA
Oy 181 LysLysSerAlaLysLysLysLysArgSerILysAlaLysGlnGluArgGluAla 200 1 1 1 1 1 1 1 1 1 1	Qy 241 SerCysValSerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGly 260	843 k or p32 prot 3587 ein.		AUTHORS Lopez-Othin.C. TILLE Direct Submission JOURNAL Submitted (08-JUN-1998) Lopez-Otin C., Bioquimica y Biologia JOURNAL Submitted (08-JUN-1998) Lopez-Otin C., Bioquimica y Biologia Molecular, Universidad de Oviedo. Facultad de Medicina., C/ Julian FEATURES Location/Qualifiers 1. 1843 Source 1. 1843 FONGARISM-"Homo saplens"	/db_xref="taxon:9606" /tissue_type="breast tumor" 1. .843 /gene="ing2" CDS 1. .984 /gene="ing2" /codon_start=1	/product="132 protein" /protein_id="CAC20567.1" /db_xref="G1:12053588" /db_xref="G1:12053588" /translation="MLGQQQQLYSSAALITGERTRILTCYVQDYLECVESLPHDWQR NYSYLRELDINXYQETHEIDDVFKYYKKEDDLNQKKRLQQLLQRALINSQELGDEKIQ IVTQMLELVENRARQMELHSQCYFODPAESERASDKAKWDSSOPERSSRRPRQRTSES RDLCHWANGIEDCDDQPPKEKKSKSAKKKRSKAKQBERASPVEFAIDPNEPTYCLCN	GRIGIN 298 a 163 c 212 g 170 t CARGINE COUNT 298 a 163 c 212 g 170 t	Alignment Scores: 7.87e-113 Length: 843 Pred. No.: 7.87e-113 Length: 843 Score: 1478.00 Matches: 279 Percent Similarity: 100.00% Conservative: 1 Best Local Similarity: 99.64% Mismatches: 0 Query Match: 99.80% Indels: 0 DB: 99.80% Indels: 0 US-09-513-365A-1 (1-280) x HSAJ6851 (1-843)

Db 608 GCATCTCTGTCGAGTTTGCCATCGATCGAGGCCCACCTACTGCTTGTGTAACCAA 667		Oy 220 ValSerTyrGlyGluMet1leGlyCysAspAsnGluGlnCysProileGluTrpPheHis 239	Db 668 GIGTCCTACGGGGAGATGATAGGCTGTGAACAATGAACAGTGTCCCATTGAATGGTTTCAC 727	010 phacartretal cart and transfer to the fired and transfer of the transfer o	240 F1GSELLYSVALSELLEULIN 17 LIYSFLOUYSGLYUYSLIPYYLYSSLOUYSCHOLYSC		Qy 260 GlyAspAsnGluLySThrMetAspLysSerThrGluLySThrLysLysAspArgArgSer 279	Db 788 GGAGACAATGAGAAAACCATGGACAAAAGTACCGAAAAGGAGAAAAGGAGAGAGGGG 847	Oy 280 Arg 280 Db 848 AGG 850	SULF 7 ING2S2	LOCUS HSING2S2 974 bp DNA linear PRI 08-SEP-2000 DEFINITION Homo sapiens p33 (ING2) gene, exon 2, complete sequence; and	complete cds. 1 AF062748 AF062748.1 GI:9992841	2 of Homo	a; Craniata; Vertebrata; E		Nagashima, M., Hagiwara, K., Minter, A.R. and Direct Submission	JOURNAL Submitted (01-MAY-1998) Laboratory of Human Carcinogenesis, National Cancer Institute, 37 Convent Dr. Bidg.37, Rm.2C26,		iens" 5"	gene order(AF062747.1:1423,1938) /qene="ING2"	mRNA join(AF062747.1:1, .239,124, .938) /gene="ING2"	/product="p33 ING2"	/godon_start=1 /product="p33"	/protein_id="AAG11396.1" /dh vrof="GT:00038/7"	/\translation=\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	IVTQMLELVENRARQMELHSQCFQDPAESERASDRAKMDSSQPERSSRRPRRQRTSES RDLCCHMANGTELECDDODODOTERERSKSRSKRKRRSKRKRGREBASPVEFALIDEPTYCLCN AUGUSTANT GENERAL STREET FROM THE	RRSH	intron <1123 /gene="ING2"	/number=1 exon 124.938	/gene="ING2" /numbe=2 polya_signal 918 .923	/gene="ING2"	BASE COUNT 348 a 156 c 205 g 265 t	Scores:	Pred. No.: 1.16e-89 Length: 974 Score: ~ 1197.00 Matches: 231
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Louis,

Fri

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Louis,
                                                                   Submitted (16-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                                                 Submitted (10-APR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                          Apr 10, 2002 this sequence version replaced g1:18677601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * NOTE: This is a 'working draft' sequence. It currently a consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                           Sequencing vector: M13; 0% Sequencing vector: M13; 0% Sequencing vector: plaamid; 100% Chemistry: Dye-primer ET; 0% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 18964b bases at least 040 Consensus quality: 190093 bases at least 020 consensus quality: 191699 bases at least 020 lineart size: 204000; agarose-fp lineart size: 1050974; sum-of-contigs Quality coverage: 10.96 in 020 bases; sum-of-contigs
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/notea-massembly_name:Contig29"
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  sequence of Homo sapiens clone

    .189972
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/db_xref="taxon:9606"

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Waterston, R.H.
                                                                                            LeuGluCysValGluSerLeuProHisAspMetGlnArgAsnValSerValLeuArgGlu 51
                                                                                                                                                                                                    LeuAspAsnLysTyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLys
                                                                                                                                                               AsnSerGlnGluLeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuVal
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Homo sapiens chromosome 4 clone RP11-367N14, WORKING DRAFT SEQUENCE, 8 unordered pieces.
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
Homo sapiens
 9000
  Conservative:
              Mismatches:
Indels:
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                                                                   x HSING2S2 (1-974)
93.98%
92.77%
80.82%
                                                                 US-09-513-365A-1 (1-280)
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Nature,

Rature,

Rat
  147293 AAATGGTATTGCCCAAAGTGCAGGGGAGATAATGAGAAAACAATGGACAAAAGTACTGAA 147352
                                                                                                                                                                                         AC128348 168245 bp DNA linear HTG 19-JUL-2002 Rattus norvegicus clone CH230-129P3, *** SEQUENCING IN PROGRESS ***, 50 unordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                147353 AAGACAAAAAGGATAGAAGATCGAGG 147379
                                                 LysThrLysLysAspArgArgSerArg 280
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HTG; HTGS_PHASE1.
Rattus norvegicus.
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Worley, K.C.
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                                                 272
                                                                                                                                                                                                                 DEFINITION
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JOURNAL
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KEYWORDS
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AC128348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysTrpTyrCysProLysCysArgGlyAspAsnGluLysThrMetAspLysSerThrGlu 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 LeuGluCysValGluSerLeuProHisAspMetGlnArgAsnValSerValLeuArgGlu 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 LeuAspAsnLysTyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLys
                                                                                                                                                                                                                                                                                                                                     700 others
                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
                                              5759. .6866
/note-"assembly_name:Contig58"
6967. .37117
/note-"assembly_name:Contig65"
37218. .101402
/note-"assembly_name:Contig66
                      'note-"assembly_name:Contig56
                                                                                                                                                                                                               vector_side:left"
101503, .189972
/note="assembly_name:Contig67
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vector_side:left"
a 40308 c 41211 g 54950 t
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1197.00
93.98%
92.77%
80.82%
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7483 others
                                                                                                                                                                                                                                                                                                                                                                      contig of 9228 bp in length
gap of unknown length
contig of 11439 bp in length
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                                                                                                                                                                                                                                                                                                                                            unknown length
of 6219 bp in length
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bp in length
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="CH230-129P3"
1 35809 c 36510 g 44464 t
                                                                                                                                                                                                                                                                            contig of 4862 b
gap of unknown 1
contig of 4606 b
gap of unknown 1
                                                                        of 3298 bunknown
                                                                                                                                                                                                                                unknown of 5139 h
                                                                                                             of 3080 lunknown
                                                                                                                                                                                                                                                                                                        gap of unknown contig of 6185
                                                                                                                                                                                                                                                                                                                          gap of unknown
contig of 6600
gap of unknown
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Matches:
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                                                                                                                                                of 4112
                                                                                                                                                               contig of 2427
gap of unknown
                                                                                                                                                                                    of 5888
                                                                                                                                                                                                      of 2671
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Best Local Similarity:
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                                                                                      NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 50 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N | but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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PheHisPheSerCysValSerLeuThrTyrLysProLysGlyLysTrpTyrCysProLys 257
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194
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Matches:
Conservative:
Mismatches:
Indels:
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  /note="ING1-like protein"
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/db_xref="GI:17864715"
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           /codon_start=1
/product="p32INGL"
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Victoria, British Columbia V8W
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                                                                                                                                                                                                                                                                                                                  GluTrpPheHisPheSerCysValSerLeuThrTyrLysProLysGlyLysTrpTyrCys 255
LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla 115
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1 (bases 1 to 1094)
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Expression of Novel ING Variants is Regulated by Thyroid Hormone
                                           ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSer
                                                                                                                                                                                                                          GlnGluArgGluAlaSerProValGluPheAlaIleAspProAsnGluProThrTyrCys
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Helbing,C.C., Wagner,M.J., Gogela-Spehar,M., Skirrow,R.C.,
Johnston,R.N. and Riabowol,K.
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J. Biol. Chem. 276 (50), 47013-47020 (2001)
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complete cds
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1. 1094
/organism="Xenopus laevis"
/db_xxef="taxon:835s"
/tissue_type="brain"
/dev_stage="tadpole"
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814 TTCATTTCTC 258 CysargGlyk 874 TGCAGAGGAG 278 ArgSerarg 2 278 ArgSerarg 3 111111111111111111111111111111111111	AC114762 Homo saplens chromosome 4 clone RP11-366M5, *** Si RPGGRESS ***, 26 unordered pieces. AC114762.2 GI:19703333 HTG; HTGS_PHASE1. Homo saplens I (bases 1 to 42029) The sequence of Homo saplens clone Unpublished I (bases 1 to 42029) Waterston, R.H. Direct Submitsion Submitted (11 xMD-2000) Commo Commonical Action Submitted (11 xMD-2000)		**NOTE: This is a 'working draft' sequence. It currently consists of 26 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as trus of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. ** In 1409

21-NOV-1999

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Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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2 (bases 1 to 840)

Garkattsev I.V.

Garkattsev I.V.

Submitted (11-MAY-1999) Genome Therapeutics Corp., 100 Beaver
Waltham, MA 02453, USA

Location/Qualifiers
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                                                            AF149820 840 bp mRNA lines
Mus musculus p33ING1 protein mRNA, complete cds.
AF149820 GI:6456561
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/organism="Mus musculus"
/d_xref="taxon:10090"
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/codon_start=1
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Mus musculus
Bukaryota; Wetazoa; Chordata; (
Mammalia; Butheria; Rodentia; 1
1 (bases 1 to 840)....., 1
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Matches:
Conservative:
Mismatches:
Indels:
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.7001
.27363. .29456
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24217. .26155
           'note="assembly_name:Contig68'
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FEATURE SO	BASE COUNORIGIN Alignment Pred. No. Score: Percent S. Best Locat Query Mat, DB: US-09-513	6 6 6 6 6	QY Db Oy	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	60 60 60 60 60 60 60 60 60 60 60 60 60 6
Qy 118 MetGluLeuHisSerGlnCysPheGlnAspProAlacluSerGluArgAla 134 :::::: ::::	19 19 19 19 19 19 19 19 19 19 19 19 19 1	RESULT 13 BC016573 LOCUS BC016573 BC016573 BC016573 BC016573 BC016573 BC016573 Inhibitor of growth family, member 1, clone MGC:27881 ACCESSION BC016573.1 GI:16741521 KEWWORDS MGC. BC016573.1 GI:16741521 KEWWORDS MCG. BC016573.1 GI:16741521 KEWWORDS MCG. BC016573.1 GI:16741521 KEWWORDS MCG. BC016573.1 GI:16741521 KEWORDS MCG. BC016573.1 GI:16741521 KEWORDS MCG. MCG. BC016573.1 GI:16741521 KEWORDS MCG. MCG. BC016573.1 GI:16741521 KEWORDS MCG. BC016573.1 GI:167	S Strausberg, T. S. Strausberg, S. S	REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov COMMENT Contact: MGC help desk Email: cgapbs.remail.nih.gov Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G. E. Consortium (LINL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Powers	Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Gontact: amg@bcm.tmc.edu Gontact: amg@bcm.tmc.edu Gontact: amg@bcm.tmc.edu Gontact: A. B. H., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, RR., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Clone distribution: M.G. clone distribution information can be found through the I.M.A.G.E. Consortium/LiML at: http://image.llnl.gov Series: IRAK Plate: 35 Row: i Column: 6.

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1221
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 840)
                                                                                                           GlyGluArgSerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSer
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                                                                                    QETLKELDDYYEKFKRETDGTQKRRVLHCIQRALIRSQELGDEKĪQIVSQMVELVENR
SRQVDSHVELFEAHQDISDGTGGSGKAGQDKSKSEAITQADKPNNKRSRRQRNNENRE
NASNNHDHDDJJSGTPKEKKAKTSKKKRRSKAKAEREASPADLPJDPNEPTYCLCNQV
SYGEMIGCDNDECPJEWFHFSCVGLNHKPKGKWYCPKCRGESEKTMDKALEKSKKERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MLSPANGEQIHLVNYVEDYLDSIESLPFDLQRNVSLMREIDAKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 2817)
Zeremski,M. HillJ.E., Kwek,S.S., Grigorian,I.A., Gurova,K.V., Garkavtsev,I.V., Diatchenko,L., Koonin,E.V. and Gudkov,A.V. Structure and regulation of the mouse ingl gene. Three alternative transcripts encode two phd finger proteins that have opposite
                                                                                                                                                 CysAspAsnGluGlnCysProlleGluTrpPheHisPheSerCysValSerLeuThrTyr 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zeremski,M., Hill,J., Garkavtsev,I.V. and Diatchenko,L.
Direct Submission
Submitted (16-AUG-1999) Molecular Genetics, Univ. of Illinois at
Chicago, 900 South Ashland Ave., Chicago, IL 60607, USA
Location/Qualifiers
                                                                AspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGly
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J. Biol. Chem. 274 (45), 32172-32181 (1999)
20011419
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Mismatches:
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/protein_id="AAF16910.1"
/db_xref="G1:6561424"
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/organ1sm="Mus musculus"
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/gene="Ing1"
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NASSNHDHDDGASGTPKEKKAKTSKKKRSKAKAEREASPADLPIDPNEPTYCLCNQV
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/translation="MLSPANGEQLHLVNYVEDYLDSIESLPFDLQRNVSLMREIDAKY
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Nagasabilma, M., Hagiwara, K., Hancock, A.R. and Harris, C.C.
Nagasabilma, M., Hagiwara, K., Hancock, A.R. and Harris, C.C.
Submitted (16-JUL-1998) Laboratory of Human Carcinogenesis,
National Cancer Institute, National Institutes of Health, 37
Convent Dr., Bldg. 37, Rm. 2Col, Bethesda, MD 20892, USA
Location/Qualifiers
Nagashima,M., Shiseki,M., Miura,K., Hagiwara,K., Linke,S.P., Pedeux,R., Wang,X.W., Yokota,J., Rlabowol,K. and Harris,C.C. DNA damage-inducible gene p331NG2 negatively regulates cell prolliferation through acetylation of p53 Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9671-9676 (2001) 21396501
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/protein_id="AAG12174.1"
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Search completed: June 20, 2003, 03:27:45 Job time: 2265 secs

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Patent No. 6403785
GENERAL INFORMATION:
TITLE OF INVENTION: Human TSC403 gene and human INGIL gene
TITLE OF INVENTION: Human TSC403 gene and human INGIL gene
TITLE OF INVENTION: Human TSC403 gene and human INGIL gene
CURRENT APPLICATION WUMBER: US/09/601,478
CURRENT FILING DATE: 2000-08-03
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-04-05
PRIOR APPLICATION NUMBER: JP H10-73234
PRIOR APPLICATION NUMBER: JP H10-38133
PRIOR FILING DATE: 1998-02-03
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Mismatches:
Indels:
Gaps:
US-09-499-082-9
US-09-258-372-9
US-09-006-783A-2
US-09-006-783A-2
US-09-109-286-2
US-09-109-286-2
US-09-109-286-3
US-09-370-838-146
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US-08-990-571-37
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US-09-528-784A-84
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SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Homo sapiens
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Best Local Similarity:
   Alignment Scores:
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LENGTH: 840
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                             nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                      ArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGluLys
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                                                                                                                                                                                          1 MetLeuGlyGlnGlnGlnGlnGlnLeuTyrSerSerAlaAlaLeuLeuThrGlyGluArg
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280
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                                                    brain cDNA library
                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                         US-09-513-365A-1 (1-280) x US-09-601-478-7 (1-1078)
                                                     embryonic
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1481.00
100.00%
100.00%
2.1
                                                   OTHER INFORMATION: human NAME/KEY: CDS LOCATION: (92)..(931)
PatentIn Ver.
                                    sapiens
                                                                 US-09-601-478-7
                                                                                                                                      Similarity:
                                                                                                                            Percent Similarity:
                         TYPE: DNA
ORGANISM: HOMO
                                                                                                   Alignment Scores:
                1078
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                                            FEATURE:
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Query Match:
        SEQ ID NO
                  LENGTH:
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	270 rGluLysThrLyslysAspargArgSerArg 280 111111111111111111111111111111111111	REFERENCE/DOCKET NUMBER: 97,837 TELEPHONE: 312-913-0001 TELEPHONE: 312-913-0001 TELEPHONE: 312-913-0002 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 873 base pairs TYPE: nucleic acid
Qy 261 AspasnGluLySThrMetaspLysSerThrGluLysThrLysLysaspargargSerarg 280	Alignment Scores:	

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GTGGACAGCCACGTGGGCGCACCAGGAGCTGGGCGACACAGTGGGCCAAC 381
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Indels:
                                                                                                                     Matches:
                                                                                                         Length:
                                                                                                                                                                    Gaps:
                                                                                                 3.74e-86
853.50
75.74%
59.19%
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Best Local Similarity:
STRANDEDNESS:
            TOPOLOGY: li
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; LOCATION:
US-09-006-783A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 TyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAsp
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136
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14
                                                                                                                    DNA SEQUENCE ENCODING A TUMOR SUPPRESSOR GENE
                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,257
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                                                                                                                                                STREET: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria STATE: Vireit
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569,721
FILING DATE: 08-DEC-1995
ATTORNEY AGENT INFORMATION:
NAME: MOO1, Leslie A.
REGISTRATION NUMBER: 37,047
                                Sequence 1, Application US/09258257 Patent No. 5965398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 0:
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                              GENERAL INFORMATION:
APPLICANT: GARKAVTSEV, IGOR
APPLICANT: RIABOWOL, KATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (650) 854-7400
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728.00
74.79%
58.12%
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                           STATE: Virginia
COUNTRY: United States
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                                                                                                                TITLE OF INVENTION: DNA TITLE OF INVENTION: SUP NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS: ADDRESSEE: BUINS DOA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION:
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RESULT 5
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DB:
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TYPE:	STRAND TOPOLO MOLECULE	FEATURE: NAME/K	LOCATI S-09-258-371	Alignment Sco Pred. No.:	Score: Percent Simil	Best Local Si Query Match: DB:	09-513-365	. 56	31	9.2	16 96	, r	116	211	131	271	144	331	164	385	184	445	204	505	224	565	244	625	264	685	RESULT 7 US-08-569-721 ; Sequence 1, ; Patent No.	GENERAL IN APPLICAN
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211 CGGCAGGTGGACAGCCACGTGGAGCTGTTCGAGGCGCAGCAGGAGCTGGGCGACACAGTG 270	SerGluArgAlaSerAspLysAlaLysMetAspSerSer	271 GGCAACAGCGGCAAGGTTGGCGGGACAGGCCCAATGGCGATGCGGTAGCGCAGTCTGAC 330	144 GlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeu 163 ::	CysHisMetalaAsnGlyIleGluAspCysAspAspGlnProProLysGluLy8LysSer	385 GCGTCCAGCAACCACGACGACGACGACGCCTCGGGCACACAAGAGAGAAGAAGAAGAAGAAGAAGAAGAAG	LysserAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal		204 GIRTHEALGISHOLDASHGIRFOIHTTYTCYSLEUCYSASHGINYALSETTYTGY ZZ3 505 GACCTCCCCAATGGACCCAGAAACCAGGATCTGYTGAACCAAGGATCTATGGG 564		565 GAGATGGCTGCGACAACGACGACGACGACCATCGAGTGCTTCCACTTCTGTGCGTG 624	244 SerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu 263	625 GGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCAAGTGCCGGGGGGAGAACGAG 684	264 LysThrMetaspLysSerThrGluLysThrLysLysLysAspArg 277	003 ANGALLAIGGALAAANGALCIIGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	-371-1 - 1 Annlination HS/00258271	Patent No. 598608 GREEN CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL OF CO	APPLICANT: Garkatsev, Igor	TITLE OF INVENTION: DAY SEQUENCE ENCODING THE TUMOR TITLE OF INVENTION: SUPPRESSOR GENE ING!	NUMBER OF SEQUENCES: 23 CORRESPONDENCE ADDRESS:	ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: 699 Prince Street	CITY: Alexandria	COUNTRY: USA ZIP: 22313-1404	8 5	COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC - DOS /MS-DOS	SOFTWARE: Patenth 1 C 2007/03 COS CHRESTON #1.30 CHRESTON ADDITION NAME 1.20	APPLICATION NUMBER: US/09/258,371 FILLING DATE.	SSI		ATTORNEY AGENT INFORMATION: NAME: MOOLY LES11E A.	STRATION RENCE/DOC	ATIC 00 1:	SEQUENCE CHARACIEKISIUCS: LENGTH: 1902 base pairs
ф	δy	qq	OY Db	٥y	qq	40 do	a &	· 경 점	^ 0	qq	٥y	Dp	Oy 40	DECITE A	US-09-258-371-1	; Paten			NO O		. •. •.		8				CLA!		, AT		INFO	, ,

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4 GlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeu 163
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Matches:
Conservative:
Mismatches:
Indels:
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nucleic acid
IDEDNESS: double
OGY: linear
                                                                  CDS
109..741
                           OGY: linear
E TYPE: cDNA
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10N:
1-1
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243

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204 GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly 223
      164 CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer 183
                                                                                LysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal 203
                                                                                                                                                                                                                                                                                                                  244 SerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu 263
                                                                                                                                                                                                                                                                                                                                                      625 GGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCAAGTGCCGGGGGGAGAACGAG 684
                                                                                                      385 GCGTCCAGCAACCACGACGACGACGCCCTCGGGCACACCCAAGGAGAAGAAGGCC
                                                                                                                                                                                   224 GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysVal
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08751230
Patent No. 6117633
GENERAL INFORMATION:
APPLICANT: Garkavtsev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: BUA SEQUENCE ENCODING THE TUMOR
TITLE OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ...orkESSEE: __ nuurESS:
STRET: 699 Prince Street
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: MOOI, LESIIE A.
REGISTRATION NUMBER: 37,047
REFERNICE/DOCKET NUMBER: 028722-144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/751,230
FILING DATE: 15-NOV-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1902 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        415-854-8275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-854-8275 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: . USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
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109..741
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; LOCATION:
US-08-751-230-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGGGCGACGAGAAGATCCAGATCGTGAGCCAGATGGTGGAGCTGGTGGAGAACCGCACG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||||||||:::::: ||| ::: |||||:::
211 CGGCAGGTGGACAGCCACGTGTTCGAGGCGCAGCAGCAGCTGGGCGACACAGTG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271 GGCAACAGCGGCAAGGTTGGCGCGGGACAGGCCCAATGGCGATGCGGTAGCGCAGTCTGAC 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 GlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeu 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 TyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAsp 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlu 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu-------
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                        ENCODING A TUMOR
                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/569,721A
FILING DATE: 08-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-513-365A-1 (1-280) x US-08-569-721A-1 (1-1902)
                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       028722-128
                      DNA SEQUENCE EN
                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MOOJ, Leslie A.
REGISTRATION NUMBER: 37,047
REPERENCE/DOCKET NUMBER: 0287;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 854-7400
TELEPAX: (650) 854-8275
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGIH: 1902 base pairs
APPLICANT: RIABOWOL, KATI
TITLE OF INVENTION: DNA S.
TITLE OF INVENTION: SUPPR
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74.798
58.128
49.168
                                                                                                                                                             STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 109..738
                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 08 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-569-721A-1
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		uAspAs 	rGlnGl	CCAGGA	nArgAl	CCCCAC	CACAGT	Serse	 GTCTGA	JASPLe	rgagaa st.::66	SAAGGCC	rProVa	CCTGC	rTyrG1	rCysva	STGCGT	AsnGl			
		TyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAsp ::::::::	AsnSe	GGGCCCAGAAGCGGCGGATGCTGCACTGTGTGCAGCGCGCGC	LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAl@ 	GAGAA	SOURCE S	MetAsı	CGCCAAGGTTGGCGCGGACACGCCCAATGCGGATAGCGCAGTCTGAC	gSerSerArgArgFroArgGhnArgThrSerGluSerArgAspLeu	AACCG	GCGTCCAGCAACCACGACGACGACGACGACGCCTCGGGCACACCCAAGGAGAAGAAGGC	LysSerAlaLysLysLysLysAgserLysAlaLysGlnGluArgGluAlaSerProVal	GCGTC(GluPheAlalieAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGl ::: 	GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysVa	TTCTC	SerLeuThrTyrLysProLysG1yLysTrpTyrCysProLysCysArgG1yAspAsnG1. 			
ო დ ღ 4. დ		TyrLys ::: TTCAG1	Leuile	CTGATO	Leuva]	CTGGTC	GAGCTO	AlaLys	 GCGGT#	Serglu	AACGAC	CCCAAC	ArgGlu	CGAGAG	AsnGlr 	PheHis	TTCCAC	CysArg	277		W
e: 339 145 2 145		luLys	rgAla	000000	euGlu	TGGAG	AGCAG	spLys	GCGAT	rgThr	GCAAC	GCACA	1nGlu	CGGAG	euCys	luTrp	AGTGG	roLys(spArd	::III	APOPTOSI:
> ::	-1902)	alTyrG	euGlnA	:: rgcAgo	InMetI	AGATGG	:: AGGCGC	laSerA	CCAATG	rgGlnA	SGCAGC	SCTCGG	laLysG	CCAAGG	rcysl 	rolleG	CATCG	rcysP	SLVSA	IIIÎI:	
Matches: Conservati Mismatches Indels: Gaps:)-1 (1	PASPV ::: CGAGT	nLeuL	CTGTG	Thre	GAGCC	GTTCG	uArgA	CAGGC	oArga	ACGGCC	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	rLysA	CAAGG	OThrT	nCysP	GTGCC	STrpT	sThrL	ATCCA	ULATI
20250	51-230	uIleAs ::: GCTAGA	uGlnG1	: GCTGC#	nIleva	GATCGI	GGAGCT	-SerG]	 GGCGG#	gArgPr	orecir.	:::!!	SArgSe	SCGCTC	nGluPr 	nGluGl	CGACGA	SGLYLY FILLI	rGluLy	GGAGAA	8
8.00 .798 .128	US-08-7	LYSG1	sArgLe	CGGAT	Illegl	SATCCA	IIII	1	SGTTGG	SerAr	AGLAA	GACCA	LysLy	SAAGAA	ProAsi 	Aspası	GACAA	ProLy	SerTh		Sequence 1, Application US/0949908; Sequence 1, Application US/0949908; Patent No. 614352 GENERAL INFORMATION: APPLICANT: Helbing, Caren C. APPLICANT: Riabowol, Karl APPLICANT: Application, Randall N APPLICANT: Garkatisev, Igor TITLE OF INVENTION: METHODS OF NUMBER OF SEQUENCES: 23 CORRESPONDENCE ADDRESS: ADDRESSEE: Burns, Doane, Swei
74.79 74.79 58.13	×	ThrLe	LysLys	AAGCGC	31uLys	GAGAAC	GACAG		SGCAAC	Argser	AAGIA	AACCAC	Lyslys	AAGAAG —	ileasi ATCGAC	31yCys	SGCTGC	FYTLYS:::	· AspLys	SACAA	DD US, DD US, DD, Rain,
/: rity:	(1-280)	SlnGlu ::::::	AsnGln	SCGCAG	lyAsp	SGCGAC	AGGTG		GGCAACAGO	GlnProGluArg	i swet	CCAGC	SerAla	CCTCC	GluPheAlail ::: GACCTCCCCAT	etile 	TGATC	euThr	hrMet	CCATG	Application Use 143522 FORMATION: T: Riabowol, T: Riabowol, T: Johnston, T: Garkavtsev Invention: Mills Secuences: Secuences: Burns, Describers, Burns, Describers, Burns, Describers, Des
larit; imila	5A-1		P ren																	S AAG	2-1 App) 61435 NFORM VT: F VT: C VT:
e: ent Similarity: Local Similari y Match:	13-36	56 31	7(91	96	151	211	131	271	4 0	164	, œ	184	44	204	224	265	244	264	685	SULT 9 -09-499-082-1 Sequence 1, A Fatent No. 61 GENERAL INFO APPLICANT: APPLICANT: APPLICANT: TITLE OF I NUMBER OF CORRESPOND ADDRESSES STREET:
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211 CGGCAGGTGGACAGCCACGTGGAGCTGTTCGAGGCGCAGCAGGAGCTGGGCGACACAGTG 270
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ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/499,082
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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PULASSIFICATION
PULASSIFICATION
PULASSIFICATION
PURBER: US/08/828,158
FILING DATE: US-MAR-1997
FILING DATE: US 08/751230
FILING DATE: 15-NOY-1996
PROR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: MOOI, LESILE A.
REFERENCE/DOCKET NUMBER: 028722-148
TELECOMMUNICATION INFORMATION:
TELECHANICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAMMUNICATION INFORMATION:
TELEFAX: 650-854-8275
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1902 base pairs
TYPE: nucled acid
STRANDEDNESS: double
TOPOLOGY: linear
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74.79%
58.12%
49.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: 109..741
US-09-499-082-1
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Best Local Similarity: 5
Query Match:
DB:
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Pred. No.:
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Score: 728.00 Matches: 136 Percent Similarity: 74.79% Conservative: 39 Best Local Similarity: 58.12% Mismatches: 45 Query Match: 49.16% Indels: 2 DB: 4 Gaps: 2	56 TyrGlnGluThrLeuLysGluIleAspAspV 56 TyrGlnGluThrLeuLysGluIleAspAspV 51 TGGAAGGTCTCTGAGGAGGAGCTAGACGAGT 76 LeuAsnGlnLysLysArgLeuGlnGlnLeuL	150 160	Qy 116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu 130	271 GGCAACAGGGGAAGGTTGGCGGACAGGCCCAATGGCGATGCGGTAGCGCAGTCTGAC 33 144 GlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeu 16 :::	Oy 164 CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer 183 ::::	Qy 184 LysSerAlaLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProval 203	Oy 204 GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly 223 :::	Qy 224 GluMetileGlyCysAspasnGluGlnCysProlleGluTrpPheHisPheSerCysVal 243	Oy 244 SerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu 263	Oy 264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277	RESULT 11 US-09-228-371-9 ; Sequence 9, Application US/09258371 ; Patent No. 5986078 ; GENERAL INFORMATION: ; APPLICANT: Garkavtsev, Igor ; APPLICANT: Riabowol, Karl ; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR ; TITLE OF INVENTION: SUPPRESSOR GENE ING1	NUMBER OF SEQUENCES: CORRESPONDENCE ADDRE: ADDRESSEE: Burns, STREET: 699 Prince CITY: Alexandria	
Db 385 GCGTCCAGCAACCACGACCACGACGCGCCTCGGGCACACCCAAGGAGAAGAAGGCC 444 Qy 184 LysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal 203	Qy 204 GluPheAlaileAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly 223 :::	244 SerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysGysArgGlyAspAsnGlu 26.	CY	; Sequence 1, Application US/09258372 ; Patent No. 6238918 ; GENERAL INFORMATION: APPLICANT: GENERAL SEQUENCE ENCODING THE TUMOR	≌ö	a %	# E E E	SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/258,372 FILING DATE:	CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/751,230 FILING DATE:	; ATTORNEY/AGENT INFORMATION: ; NAME: Mooi, Leslie A. ; REGISTRATION NUMBER: 37,047 ; REFERENCE/DOCKET NUMBER: 028722-144	INFORMATIC 354-7400 1-8275 ID NO: 1: ESTICS: Se pairs sid ouble	MAME/KEY: CDNA NAME/KEY: CDS LOCATION: 109.741	Alignment Scores: 1.2e-71 Length: 1902

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243
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                       204 GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly
                                                                           GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysVal
                                                                                                                                                                                                                              Sequence 9, Application US/08751230
Patent No. 6117633
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Garkavisev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
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Mismatches:
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Matches:
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SOFTWARE: PATENTIN Release #1.0, Vej
CURRENT APPLICATION DATA: US/08/751,230
FILING DATE: 15-NOV-1996
CLASSIFICATION 514
PRIOR APPLICATION DATA: 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY AGENT INFORMATION: NAME: MOOJ, Leslie A. REGISTRATION NUMBER: 37,047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION
TELEPHONE: 415-854-7400
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728.00
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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STATE: VACCOUNTRY:
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370 CGGCAGGTGGACACCACGTGTTCGAGGCGCAGAGGTGGGCGACACACAGTG 429
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               TYPE: Floppy disk
ER: IBM PC| compatible
ING SYSTEM: PC-DOS/MS-DOS
RE: Patentin Release #1.0, Version #1.30
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                      028722-144
                               COMPUTER: IBM PC compatible OPERATING SYSTEM; PC-DOS/MS-DOS SOFTWARE: PETENTIN Release #1.0, CURRENT APPLICATION DATE: US/09/258,371
                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MOOI, LESIDE A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 0287
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
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TYPE: nucleic acid
STRANDEDNESS: double
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74.798
58.128
49.168
COMPUTER READABLE FORM:
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Best Local Similarity:
Query Match:
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US-09-258-371-9
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APPLICATION NUMBER: US/09/499,082
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US-09-499-082-9
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                                                                                                                                                                                                                                                                                                                  164 CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer
                              GluPhealaIleaspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly :::
                                                                                                                                                                                                                                                                                                                                                                                                      GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysVal
           TyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAsp
                                                      LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlu
                                                                                                                                          ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu-------
                                                                                                                                                                                    -----SerGluArgAlaSerAspLysAlaLysMetAspSerSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9. Application US/09499082;
Patent No. 6143522;
GENERAL INFORMATION:
APPLICANT: Riabowol, Karl
APPLICANT: Riabowol, Karl
APPLICANT: Garkavtsev, Igor
TILLE OF INVENTION: METHODS OF MODULATING APOPTOSIS;
NUMBER OF SEQUENCES:
ADDRESSONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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STREET: 699 Prince Street
CITY: Alexandria
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COMPUTER: IBM PC compatible
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CURRENT APPLICATION DATA:
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Mismatches:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 27-WAR-1997
APPLICATION NUMBER: US 08/751230
FILING DATE: 15-NOV-1996
FILING DATE: 15-NOV-1996
FILING DATE: 15-NOV-1996
FILING DATE: 10-NOV-1996
FILING DATE: 10-NOV-1996
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 0.28722-148
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFOR
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96 LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla 115
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370 CGGCAGGTGGACAGCCAGTGGTGTTCGAGGCGCAGCAGGAGCTGGGCGACACAGTG 429
                                                                                                                                                                                                                                                                   --SerGluArgAlaSerAspLysAlaLysMetAspSerSer 143
                                                                                                                                                                                                                                                                                                                                     GlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeu 163
                                                                                                                                                                                                                                                                                                                                                                                                   164 CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      784 GGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCAAGTGCCGGGGGGGAACGAG 843
 75
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GACCTCCCCATCGACCCCAACGAACCCACGTACTGTGTGCAACCAGGTCTCTATGG
                    56 TyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAsp
                                                                 76 LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlu
                                                                                                                                                                                                   116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu-------
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; Patent No. 6420136
; GENERAL INFORMATION:
APPLICANT: RIABOWOL, Karl T.
TITLE OF INVENTION: METHOD OF MODULATING P53 ACTIVITY
FILE REFERENCE: 028722-181
; CURRENT APPLICATION NUMBER: US/09/159,871A
; CURRENT APPLICATION NUMBER: US 60/060,138
; PRIOR APPLICATION NUMBER: US 60/060,138
; PRIOR APPLICATION NUMBER: US 60/066,783
; PRIOR FILING DATE: 1998-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
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SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (16)..(897)
US-09-159-871-1
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ORGANISM: Human
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                                                                 GluMetIleGiyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysVal
                                                                                                                                     784 GGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCAAGTGCCGGGGGGAAAAGAACGAG
                                                                                                                                                                              264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
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136
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APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE ING!
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: MOOJ, Les/life A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-1
TELEPHONE: 415-854-800
                                                                                                                                                                                                                                                                              Sequence 9, Application US/09258372
Patent No. 6238918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-854|-8275
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2061 base pairs
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74.79%
58.12%
49.16%
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ZIP: 22313-1404
COMPUTER READABLE FORM:
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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Pred. No.:
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US-09-258-372-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: V. COUNTRY:
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US-09-258-372-9
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2061 136 : 39 145 2		TyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAsp	TGGAAACAGATCCTGAAGGAGCTAGACGAGTGCTACAGGAGCGCTTCAGTCGCGGGAGCAGC	rgAlaLeuIleAsnSerGlnGlu	GGGCCCAGAAGCGGCGGATGCTGCACTGTGTGCAGCGCGCGC	euGluLeuValGluAsnArgAla	CTGGGCGACGACGAGAAGATCCAGATCGTGAGCCAGATGGTGGAGCTGGAGAACCGCACG	roAlaGlu	CGGCAGGTGGACACCACGTGGAGCTGTTCGAGGCGCACCAGGAGCTGGGCGACACAGTG	SerGluArgAlaSerAspLysAlaLysMetAspSerSer	GCGATGCGGTAGCGCAGTCTGAC	GlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeu	AACAGCAAGCGCTCACGCGGCAGCGCAACAACAGAACCGTGAGAAC	CysHisMetalaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer	GCGTCCAGCAACCACGACCACGACGCGCGCGTCGGGCACACCCAAGGAGGAGGAGGCC	LysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal	CGGAGCGAGGCGTCCCCTGCC	GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly	TGTGCAACCAGGTCTCCTATGGG	GluMetileGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysVal	AGTGGTTCCACTTCTCGTGCGTG	SerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu	GGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCAAGTGCCGGGGGGGAACGAG	spArg 277	AGAGG 885
Length: Matches: Conservative Mismatches: Indels:	59-871-1 (1-2061)	IleAspAspValTyrG	::: CTAGACGAGTGCTACG	GlnGlnLeuLeuGlnA	::: SCTGCACTGTGTGCAGC	IleValThrGlnMetL	SATCGTGAGCCAGATGG	ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu	GAGCTGTTCGAGGCGC	SerGluArgAlaSerA	GCGGACAGGCCCAATG	ArgProArgArgGlnA	GGCTCACGCCGCCAGC	GluAspCysAspAspG	GACGACGCGCGTCGG	ArgSerLysAlaLysG	GGCTCCAAGGCGAAGG	GluProThrTyrCysLe	GAACCCACGTACTGTC	GluGlnCysProIleG	GACGAGTGCCCCATCG	GlyLysTrpTyrCysP	GGCAAGTGGTACTGTC	LysThrMetAspLysSerThrGluLysThrLysLysAspArg	GAGAATCCAAAAAGG
1.35e-71 728.00 74.79% 1ty: 58.12% 49.16%	1-280) x US-09-159	lnGluThrLeuLysGlu	aacagatcctgaaggag	snGlnLysLysArgLeu	CGCAGAAGCGGCGGATG	lyAspGluLysIleGln	GCGACGAGAAGATCCAG	InMetGluLeuHisSer	AGGTGGACAGCCACGTG		ACAGCGGCAAGGTTGGC	roGluArgSerSerArg	CCAACAGCAAG	isMetAlaAsnGlyIle	CCAGCAACCACGACCAC	erAlaLysLysLysLys	CCTCCAAGAAGAAGAAG	heAlaIleAspProAsn	rcccarcgacccaac	etIleGlyCysAspAsn	rgatcggctgcgacaac	euThrTyrLysProLys	CAATCATAAACCCAAG	hrMetAspLysSerThr	CATGGACAAAGCCCTG
Scores: milarity Similar h:	5A-1 (1																								
hent No.: nt Si Accal	9-513-365	26	190	9,2	250	96	310	116	370	131	430	144	490	164	544	184	604	204	. 664	224	724	244	784	264	844
Alignm Pred. Score: Percen Best L Query DB:	0-SD	Qy	qq	٥y	qq	οy	qq	δy	QQ	οy	đ	Oy	g	ογ	q	ΟŸ	Q	ογ	ор	οy	QQ	ΟŸ	QQ	οy	Ω

Search completed: June 20, 2003, 03:51:30 Job time: 81 secs

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Sequence 2, Appli
Sequence 37033, A
Sequence 435, App
Sequence 146, App
Sequence 146, App
Sequence 1178, App
Sequence 277, App
Sequence 277, App
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Sequence 471, App
Sequence 142, App
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Sequence 325, App
Sequence 17120, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVESTIGATION Human TSC403 gene and human INGIL gene
TITLE OF INVESTIGANI: 060193
FILE REFERENCE: 060193
CURRENT APPLICATION NUMBER: US/10/115,899
CURRENT FILING DATE: 2002-04-05
FRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 12000-08-03
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-04-05
PRIOR FILING DATE: 1998-03-05
PRIOR FILING DATE: 1998-03-05
PRIOR FILING DATE: 1998-02-03
NUMBER OF SEQ ID NOS: 11
SOFFWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human embryonic brain cDNA library
US-10-115-899-6
                                                                                                                      12 US-09-918-995-16647

12 US-10-044-090-370

10 US-09-764-864-471

9 US-10-175-523-142

10 US-09-867-701-2399

9 US-10-072-094-96

9 US-09-286-488-17

9 US-09-853-079-17

10 US-09-737-178-17

10 US-09-737-178-17
US-09-968-653A-2
US-09-968-653A-6
US-10-037-270-33
US-10-037-270-435
US-09-854-133-146
US-09-938-842A-1178
US-09-9801-368-257
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US-09-853-079-143

0 US-09-853-079-143

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0 US-09-853-079-86

US-10-072-094-98

US-10-072-094-97

US-10-173-539-1

US-10-173-539-13

US-10-173-539-14

US-10-173-539-14
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US-09-962-436-288
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   722
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474
359
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277.5
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130.5
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Sequence 7, Appli
Sequence 4, Appli
Sequence 3454, Ap
                                                                                                                         (without alignments)
2567.998 Million cell updates/sec
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1481
1 MLGQQQQLYSSAALLTGER......DNEKTMDKSTEKTKKDRRSR
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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4: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
                                                                                                           ; Search time 160 Seconds
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/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-764-877-3454
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US-10-115-899-7
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0, Xgapext C
Ygapop 10.0, Ygapext C
Fgapop 6.0, Fgapext
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                                                                                            ATGTTAGGGCAGCAGCAGCAACTGTACTCGTCGGCCGCGCGCTCCTGACCGGGGAGCGG
                                                                                                           SerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuProHis
                                                                                                                                          AspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeu
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Patent No. US20020151025A1
GENERAL INFORMATION:
APPLICANT: Ostuka Pharmaceutical Co., Ltd.
TITLE OF INVENTION: Human TSC403 gene and human INGIL gene
       840
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      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                            US-09-513-365A-1 (1-280) x US-10-115-899-6 (1-840)
     4.4e-162
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                    Percent Similarity:
Best Local Similarity:
Alignment Scores
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Indels:
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CURRENT APPLICATION NUMBER: US/10/115,899
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 09/601,478
PRIOR APPLICATION NUMBER: 1996-0134679
PRIOR PILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: JP H10-134679
PRIOR PILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-03-05
PRIOR FILING DATE: 1998-03-05
PRIOR FILING DATE: 1998-02-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENT NOS: 11
SOFTWARE: PATENT NOS: 11
SOFTWARE: PATENT NOS: 11
SEQ ID NO 7
LENGTH: 1078
                                                                                                                                                                                                                                     OTHER INFORMATION: human embryonic brain
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                                                                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: (92)..(931)
US-10-115-899-7
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Best Local Similarity:
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                                                 GlyGluArgSerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSer
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Patent No. US20020147140A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 3454
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                                TCACCTGTTGAGTTTGCAATAGATCCTAATGAACCTACATACTGCTTATGCAACCAAGTG
                                                            SerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheH1sPhe
                                                                              TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling Pathway
                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
STSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Matches:
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NAME: NO. USZO030073064Alnan, Kevin
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 97,837
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/006,783A FILING DATE: 15-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/968,653F
FILING DATE: 01-Oct-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels:
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SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                        Sequence 4, Application US/09968653A Publication No. US20030073084A1 GENERAL INFORMATION:
APPLICANT: Gudkov, Andrey V Garkavstev, Igor Ralbowoll, Karl
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75.74%
59.19%
57.63%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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Query Match:
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Pred. No.:
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NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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                                                 CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
                                                                          COUNTRY: USA
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeuCysHisMetAla 167
                                                                                                                                                                                      GluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsn 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 AsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSerLysSerAlalys
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6592 CACGACCACGACGACGCCTCGGGCACACCCAAGGAGAAGAAGGCCAAGACCTCCAAG
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                                                                                                                                                                                                                                                                                                                                                                                       137 LysAlaLysMetAspSerSerGlnPro------GluArg
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                                                                                                                                                             US-09-513-365A-1 (1-280) x US-09-764-877-3454 (1-8487)
                                                                                                 Conservative:
Mismatches:
Indels:
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Matches:
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Riabowol, Karl
                                                                 1.93e-73
728.00
75.22%
59.13%
          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3454
                                                                                               Percent Similarity:
Best Local Similarity:
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                                                           Alignment Scores:
Pred. No.:
LENGIH: 8487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 GlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeu 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         490 AAGCCC-----AACAGCAAAGCGCTCACGGCGGCAGCGCAACAACGAGAACCGTGAGAAC
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ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff STREET: 300 South Wacker Drive
                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/968,653A
FILING DATE: 01-Oct-2001
CLASSIFICATION: <Unknown>
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135
39
46
14
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APPLICATION DATA:

APPLICATION NUMBER: US/09/006,783A
FILING DATE: 15-0An-1998
ATTORNEY/AGENT INFORMATION:

NAME: NO. US20030073084A1nan, Kevin E REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 97,837
TELECOMMUNICATION INFORMATION:

TELERAN: 312-913-0002
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Matches:
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SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                           MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
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722.00
74.36%
57.69%
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Alignment Scores: 2.04e-67 Length: 633 Fred. No.: 662.00 Matches: 125 Score: 75.49% Conservative: 29 Best Local Similarity: 61.27% Mismatches: 36 Query Match: 44.70% Indels: 14 DB: 9 Gaps: 2	Oy 86 LeuGlnargAlaLeulleAsnSerGlnGluLeuGlyAspGluLysIleGlnIleValThr 105 :::	Oy 126 GlnAspProAlaGlu	Oy 154 ArgGlnArgThrSerGluSerArgAspLeuCysHisMetAlaAsnGlyIleGluAspCys 173	194 AlaLysGlnGluArgGluAlaSerProvalGluPheAlaIleAspProAsnGluProThr 21	Oy 234 ProlleGluTrpPheHisPheSerCysValSerLeuThrTyrLysProLysGlyLysTrp 253	Oy 274 LysLysAspArg 277 :: Db 607 AAAAAGAGG 618 RESULT 7 US-09-918-995-37033 Sequence 37033, Application US/09918995	; Publication No. U\$20030073623A1 ; GENERAL INCVEMATION: APPLICANT: Hyseq. Inc. TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: RROW VARIOUS CDNA LIBRARIES FILE REFERENCE: 20411.756 ; CURRENT APPLICATION NUMBER: U\$/09/918,995 ; CURRENT APPLICATION NUMBER: U\$/09/235,076 ; PRIOR APPLICATION NUMBER: U\$/09/235,076 ; PRIOR FILING DATE: 1999-01-20 ; NUMBER OF SEQ ID NOS: 38054 ; SOFTWARE: FastSEQ for Windows Version 3.0 ; SEQ ID NO 37033 ; LENGTH: 421
164 CysHisMetalaAsnGlylleGluAspCysAspAspGlnProbroLysGluLysLysSer 183 ::::	GluMetileGlyCysaspasnGluGlnCysProlleGluTrpPheHisPheSerCysVal 24 GluMetileGlyCysaspasnGluGlnCysProlleGluTrpPheHisPheSerCysVal 24 [Andresinisicceandroceeeeee	CENERAL INFORMATION: 0.72003007308411 GENERAL INFORMATION: 0.72003007308411 GENERAL INFORMATION: 0.72003007308411 GENERAL INFORMATION: 0.72003007308401 0.72003007308401 0.72003073081 0.7200307	E SEQUENCES: NDENCE ADDRE RESSEE: McDo SET: 300 Sou SET: Chicago IE: Illinois NTRY: USA : 60606	COMPUTER KEALABLE FUOPPY disk MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/968,653A FILLING DATE: 01-OCC-2001 CLASSIFICATION: VUNKNOWN>	PRIOR APPLICATION DATA: APPLICATION NUMBER: US/09/006,783A FILING DATE: 15-JAN-1998 ATTORNEY/AGENT INFORMATION: NAME: NO. US2003073084Alnan, Kevin E REGISTRATION NUMBER: 35,303 REFERENCE/DOCKET NUMBER: 97,837	

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Pred. No.:
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APPLICANT: Ashnay, Vinod
APPLICANT: Ashnay, Vinod
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong
APPLICANT: Town, Qing A.
APPLICANT: Wehrman, Town
APPLICANT: Wang, Yonghong
APPLICANT: Yang, Yonghong
APPLICANT: Zhou, Ping
APPLICANT: Wang, Yunging
APPLICANT: Wang, Lining
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Dinorui
APPLICANT: Wang, Chiwei
APPLICANT: Prinanac, Radoje T;
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 704C1P2B
CURRENT FILING DATE: 2002-01-04
PRIOR PILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 2000-01-21
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Mismatches:
Indels:
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Matches:
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; Sequence 435, Application US/10037270
; Publication No. US20030104529A1
; GENERAL INFORMATION:
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SOFTWARE: PL_FL_genes Version 1.0
SEQ ID NO 435
LENGTH: 1864
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474.00
90.008
85.008
32.018
                                                       ; LOCATION: (1)...(421)
; OTHER INFORMATION: n = A,T,C
US-09-918-995-37033
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APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Chen, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Tang, Qing A.
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Yang, Yonghong
APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
TYPE: DNA
ORGANISM: Homo sapiens
                                          NAME/KEY: misc_feature
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    272 -----GATCAACTAGAACAAGAGTCAGTGAATTCTTTATGAATGCAAAGAAAAT 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 AAACCTGAGTGGAGGGAAGAGCAAATGGCATCCATCAAAAAGACTACTATAAAGCTTTG 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             563 AACAATCACCATGCTCATTCACATACTCCAGTGGAAAAAAGGAAATATAATCCAACTTCT
                                                                                                                                                                                                                                                                                                                                                      22 ArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuProHisAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 CTGCGGGACCGCTTCACGGAAATGCGCGAGATGGACCTGCAGGTGCAGAATGCAATG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 GluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLysLys---
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102
53
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1198
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                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                             US-09-513-365A-1 (1-280) x US-10-037-270-435 (1-1864)
                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                     1.18e-31
359.00
34.22%
22.52%
24.24%
                                           ; NAME/KEY: CDS
; LOCATION: (164)..(1420)
US-10-037-270-435
ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                         Similarity:
                                                                                                                                                                                              Percent Similarity:
Best Local Similari
                                                                                                                                   Alignment Scores:
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                                                                                                                                                                                                                                                Query Match:
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Oy 55 LysTyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAsp 74	75 AspleuAsnGlnlysLysArgLeuGlnClnLeuLeuGlnArgAlaLeuIleAsnSerGln 94 11	Qy 95 GluLeuGlyAspGluLySIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArg 114	Oy 115 AlaargGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGluSerGluArg 133	Oy 134 AlaSerAspLysAlaLysMetAspSerSerGlnPro	Oy 146GluargSerSerargargProArgargGlnargThrSerGluSerargasp 162 ::: ::: :::	RESULT 10 US-09-738-973-146 ; Sequence 146, Application US/09738973	; FACENL NO. US-COLOULIUS SALL ; FACENL INFORMATION: APPLICANT: Reed, Steven G. ; APPLICANT: Henderson, Robert A.	; APPLICANT: Lodes, Michael J. ; APPLICANT: Fling, Steven P. ; APPLICANT: Mohamath, Raodoh ; APPLICANT: Algate, Paul A.	; APPLICANT: Secrist, Heather ; APPLICANT: Indirias, Carol Yoseph ; APPLICANT: Benson, Darin R. ; APPLICANT: Polity Mark	APPLICANT: BILLOU, MAIN APPLICANT: Mannion, Jane APPLICANT: Malos, Michael D. TITIE OF INVENTION: COMPOSITIONS AND WETHODS FOR	; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER ; FILE REFERENCE: 210121.475C9 ; CURRENT APPLICATION NUMBER: 108/09/738,973 ; CHIED THE CANCENT DAME: 2000.12-14	CONTENT FILTER DATE: 2000-12-14 NUMBER OF SEQ ID NOS: 587 SOFTWARE: FastSEQ for Windows Version 3.0 SEO ID NO 146	; LENGTH: 451 ; TYPE: DNA ; ORGANISM: Homo sapien US-09-738-973-146		: 49.28% Mismatches: 21.20% Indels: 10 Gaps:	US-09-513-365A-1 (1-280) x US-09-738-973-146 (1-451)	Oy 35 ValGluSerLeuProHisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsn 54 :::	Qy 55 LysTyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAsp 74	// MARIALLARGANGILCIGARGGGGGCIAGGGGCGCIILGGGGGGGGGGGGGGGGGGGGGG
Qy 160SerArgAspLeuCysHisMetalaAsnGlyIleGluAspCysAspAspGlnPro 177	178 ProlysGlulysLysSerlysSerAlalysLysLysLysArgSerLysAlalysGluGlu ::: :: ::::: ::::: ::::: ::::: ::::: ::::: ::::::	Oy 198 ArgGluAla	Qy 201	Qy 206 AlaileAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMet 225	Qy 226 IleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysValSerLeu 245 :::	Oy 246 ThrTyrLysPholysGlyLysTrpTyrCysProLysCys	Qy 260 GlyAspAsnGluLysThrMetAspLysSerThrGluLysThr 273	Qy 274bysLysAspArgArgSerArg 280 Db 1463 GATTTATATAGGACTTTAAAAGAAGAAGAAGA 1501	RESULT 9 US-09-854-133-146 Sequence 146 Application IIS/A0854133	; Publication No. US20020183499A1 ; GENERAL INFORMATION: ; APPLICANT: Lodes, Michael J.	; APPLICANT: Mohamath, Raodoh ; APPLICANT: Henderson, Robert A.; ; APPLICANT: Benson, Darin R.	; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER ; FILE REFERENCE: 210121.475C10	CURRENT APPLICATION NUMBER: US/09/854,133 CURRENT FILING DATE: 2001-05-11 NUMBER OF SEQ ID NOS: 735 SOFTWARE: FastSEQ for Windows Version 3.0	; SEQ ID NO 146; ; LENGTH: 451 ; TYPE: DNA ; ORCANISM: Homo sapien US-09-854-133-146	7 Length:	t Similarity: 70.29%	21.20% Indels: 9 Gaps:	US-09-513-365A-1 (1-280) x US-09-854-133-146 (1-451) Qy 35 ValGluSerLeuProHisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsn 54	Db 17 ATCGAGTCCCTGCCTTCGACTTGCAGAAATGTCTCGCTGATGCGGGAGATCGACGCG 76

Db 137 GACGGGCGCAAAGCGGCGGAFGCTGCACTGCACGCGCGCATGATCCCAACACAAAGCGCGCAAAGCGCGCGGAFGCTGCACTGCA	
11	111 ValGluAsnArgAlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu
115	DD 289 AFAGATGATGAAAACGACFIGATGAAGAFCTGAATAATTTGCAGAA 339 Ov 131 SerGluargalaSerAsoLvsAlaLvsMetAspSerSerGln
256 ACGCGGCAGGTGGACCACGTGGAGCTGTTCGAGGCGCAGCAGCAGCAGCACACA	340 GATTTAAAGCAAAAAATTCCACCAGACGCCTCTGTTCTTCCTCCACTACCT
Oy 134 AlaSerAspLysAlaLysMetAspSerSerGlnPro	145ProGludrgSerSerArgArg-ProArgArgGlnArgThrSerGluSerArgAs
7	400 ATAGITCCIAAAGCGGAAAAGCGIAAGICCITCIATGGCACACACCICAGCAAGAATI
Oy 146GluargSerSerArgargProArgArgGlnargThrSerGluSerArgasp 162	Qy 162 pLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGl 180 :::
RESULT 11 US-09-938-842A-1178 ; Sequence 1178, Application US/09938842A ; Datest No resolution to the content of the content o	Qy 180 uLysLysSerLysSeralaLysLysLysArgSerLysAlaLysGlnGluArgGluAl 200 :::::: Db 514
GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Harper, Jeff APPLICANT: Kreps, Joel	Qy 200 aSerProValGluPhealaileAspProAsnGluProThrTyrCysLeuCysAsnGl 219
APPLICANT: Many Conference of Transferice Containing TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE	Qy 219 nValSerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPh 238
. 22 4 2 5	Qy 238 eHisPheSerCysValSerLeuThrTyrLysProLysGlyLysTrp 253
FRIOR APPLICATION NUMBER: US 60/264,647 PRIOR FILING DATE: 2001-01-16 PRIOR PELLING DATE: 2001-01-16 PRIOR PELLING NUMBER: US 60/300,111 PRIOR PETING NUMBER: US 60/300,111	RESULT 12 US-09-801-368-257 ; Sequence 257, Application US/09801368
; NUMBER OF SEQ ID NOS: 5379 ; SEQ ID NO 1178 : LENGTH: 813	; FACELL NO. USZUZZUZZSZUAI ; GENERAL INFORMATION: ; APPLICANT: Busby, Robert . ADBITCANT: Cali Priso
TYPE: DNA CORGANISM: Arabidopsis thaliana US-09-938-842A-1178	; APPLICANT: Hecht, Digit ; APPLICANT: Holtzman, Doug ; APPLICANT: Madden, Kevin
9.79e-23 Length: 277.50 Matches: 45.35% Conservative:	; APPLICANT: Maxon, Mary ; APPLICANT: Milne, Todd ; APPLICANT: No. US20020128250Alman, Thea ; APPLICANT: Royer, John : APPLICANT: Salama, Sofie
Mismatches: Indels: Gaps:	; APPLICANT: Sherman, Amir ; APPLICANT: Silva, Jeff ; APPLICANT: Summers, Eric
US-09-513-365A-1 (1-280) x US-09-938-842A-1178 (1-813)	; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi ; FILE REFERENCE: 109272.147
Qy 27 TyrValGlnAspTyrLeuGluCysValGluSerLeuProHisAspMetGlnArgAsnVal 46 	CURRENT AFFILMS DATE: 2001-03-07; PRIOR APPLICATION NUMBER: US 09/487,558 ; PRIOR FILING DATE: 2000-01-19
QY 47 SerValLeuArgGluLeuAsp53 ::::::	; PRIOR APPLICATION NUMBER: US 60/160,587 ; PRIOR FILING DATE: 1999-10-20 ; NUMBER OF SEO ID NOS: 440 ; SOFTWARE: Patentin version 3.0
Qy 54AsnLysTyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyr 70	; SEO ID NO 257 ; LENGTH: 993 ; TYPE: DNA ; ORGANISM: Saccharomyces cerevisiae
Oy 71 LysLysGluAspAspLeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeu 90	1 con 4 + h ·
91 IleAsnSerGlnGluLeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeu 1	Fred. No.: 5.40e 21 Lengun: 575 Score: 263.50 Matches: 75 Percent Similarity: 37.04% Conservative: 45

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Best Local Si Query Match: DB:	Similarity: 23.15% Mismatches: 17.79% Indels: 10 Gaps:	les: 105 99 8	RESULT 13 US-09-918-9
US-09-513-36	-365A-1 (1-280) x US-09-801-368-257 (1	(1-993)	; Sequence ; Publication
Oy 28 Db 31	ValGlnAspTyrLeuGluCysValGluSerLeuProHisAspMetGlnArgAsnValSer :::	ProHisaspMetGlnargasnValSer 47 	_
Qy 48		ThrLeuLysGlulleAspAspValTyr 67 :::::: TCTATGCGAATTTGAACGAGGATA 150	; FILE REFI ; CURRENT ; CURRENT ; ; PRIOR API
Qy 68 Db 151			0,
Oy 78			; LENGTH: ; TYPE: DI ; ORGANISI
			; FEATURE ; NAME/KE; ; LOCATIOI ; OTHER II US-09-918-91
0y 118			Alignment So
310	::: TTAGAATTGGCGTATGAAGTCGCAATCAAGAACACAGAAATTCCTAGAGGTTTAAGACTG	ACAGAAATTCCTAGAGGTTTAAGACTG 369	Score:
Oy 121 Db 370	GGTGTGGACAA	-HisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAsp 136 CATCCAGCAATGCACCTCCATGAACTAATGGAAAAAATAGAGAGC 429	Percent Sam: Best Local (Query Match DB:
Qy 137		ArgSerSerArgArgPro 152	US-09-513-3
Db 430	AAATCAAACAGCAAATCGTCGCAGGCACTG		δδ
Oy 153	ArghrgGln	ArgThrSerGluSerArg 161 ::: ::: AGCACACAAAAGACGACTCAAAG 549	a è
Oy 162			
Db 550	::: AACGACGCAAACTACGGAGGCAGGAGGCGAGGAGGCCAAGACCACACTGGTAACAACACA	 AGCCAAGACCACACTGGTAACAACACA 609	QY
Qy 182	LysSer	SerAlaLysLys 188	.1 qa 1.
Db 610		AACAACGCCGATCCAGAGACCAAAAAA 669	Qy
Oy 189	LysLysArgSerLysAlaLysGlnGluArgGluAlaSerProValGluPheAlaIle- 	AlaSerProValGluPheAlaIle 207	.5 Db 2:
Db 670	ဗ	CCAAGCACTATCAGCACGGCAACTGCC 729	0y · 1(
			. Db 29
Db 730) GTCAATAATGGCAGGATAGGTACATCTACAGGGGTCCAGGGGAGTTAGCAGCGTCGGAAAC	TCCAGGGGAGTTAGCAGCGTCGGAAAC 789	. Oy 1:
		AspProAsnGluProThrTyrCys 215	e qu
Db 790) AGCAACAACAGGATATCAAGACCAAAAACCAACGACTACGGCGAACCGCTCTACTGC	AACGACTACGCCGAACCGCTCTACTGC 849	0y 1,
Qy 216	LeuCysAsnGlnValSerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysProIle	GlyCysAspAsnGluGlnCysProlle 235	Db 36
Db 850		segretaresecadacieraacia 909	RESULT 14
Qy 236 Db 910	GluTrpPheHisPheSerCysValSerLeuThrTyrLysProLysGlyLysTrpTyrCys	TyrLysProLysGlyLysTrpTyrCys 255 	; Sequence ; Patent No ; GENERAL II
	256 ProLysCysArg 259		; APPLICANY ; TITLE OF ; FILE REFI
DD 97(GACGACTGCAAA 981		l ; CURRENT !

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NT: Olga Bandman
F INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FEBRENCE: PA-0028 US
APPLICATION NUMBER: US/10/044,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 GCTGCAGAGTACATCTCCACGTGAAGACGCTGTCCAGACCAGCGCGTGGAGCGCCTG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299 GCCATGCAGACCTACGAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCG 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 ValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGluLeuHisSerGln 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 TyrGluLysTyr---LysLysGluAspAspLeuAsnGlnLysLysArgLeuGlnGlnLeu 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 TyrValGlnAspTyrLeuGluCysValGluSerLeuProHisAspMetGlnArgAsnVal 46
                                                              ICANT: Hyseq, Inc.

E OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

E OF INVENTION: FROM VARIOUS cDNA LIBRARIES

REFERENCE: 20411-756

ENT APPLICATION NUMBER: US/09/918,995

ENT FILING DATE: 10909-01-20

R APPLICATION NUMBER: US/09/235,076

R FILING DATE: 1999-01-20

R FILING DATE: 1999-01-20

R FILING DATE: 1999-01-20

R ARRE: FastSEQ for Windows Version 3.0

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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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ion No. US20030073623A1
INFORMATION:
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o. US20020137081A1
INFORMATION:
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ON: (1)...(456)
INFORMATION: n = A,T,C or G
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54.69%
30.47%
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195-16047
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ORGANISM: Homo sapiens

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                                                                                                                                                                                                                                                                                                                                                                                                    122 SerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMetAsp 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 PheHisPheSerCysVal----SerLeuThrTyrLysProLysGlyLysTrpTyrCys 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 SerSerGlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArg 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 AspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLys 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LysSerLysSerAlaLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSer 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 AsnGlnValSerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysProIleGluTrp 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----AsnGluLysThrMetAspLysSer 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 ProValGluPheAlaIleAspProAsnGlu-----ProThrTyrCys---LeuCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1650 CAGCAG-----GGTGGGGAAATTATTCTGTGTGACACC-----TGCCCT---CGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1476 AGTGGCAGTGTCCACAGTGCCTCAGGCCGGCCT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 471, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT23
CURRENT APPLICANTE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARR: Patentin Ver. 2.0
SEQ ID NO 471
                                                                                                                                               ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 235885.5
US-10-044-090-370
                                                                                                                                                                                                                                         7805
446
20
66
39
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Mismatches:
Indels:
Gaps:
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Matches:
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CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 370
LENGTH: 7805
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130.50
38.60%
26.90%
8.81%
                                                                                            TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity:
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Mismatches:
Indels:
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NAME/KEY: SITE
LOCATION: (894)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: SITE
LOCATION: (903)
OTHER INFORMATION: n equals a,t,g, or
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US-09-764-864-471
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Best Local Similarity:
Query Match:
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Patent No. 6403785

GENERAL INFORMATION:
APPLICANT: Ostuka Pharmaceutical Co., Ltd.
TITLE OF INVENTION: Human TSC403 gene and human INGIL gene
FILE REFERENCE: 060193

CURRENT APPLICATION NUMBER: US/09/601,478

CURRENT APPLICATION NUMBER: JP H10-134679

PRIOR FILING DATE: 1998-04-28

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: JP H10-73234

PRIOR APPLICATION NUMBER: JP H10-73234

PRIOR APPLICATION NUMBER: JP H10-73234

PRIOR FILING DATE: 1998-03-05

PRIOR FILING DATE: 1998-03-05

WUMBER OF SEQ ID NOS: 11
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Pred. No. 1.4e-264;
       US-09-298-568-1

US-08-770-379-20

US-08-777-69A-20

US-09-230-371A-20

US-09-208-742-3

US-09-208-742-3

US-09-385-982-251

US-08-956-307B-11

5198345-16

US-09-004-731-42

US-09-032-215-46

US-08-749-699-40
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Best Local Similarity 99.5
Matches 1049; Conservative
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US-09-601-478-7
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LENGTH: 1078
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
       version 5.1.6 - 2003 Compugen Ltd
                                                                  June 20, 2003, 01:21:09 ; Search time
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                                                nucleic search, using sw model
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                 TGAAAAAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAAATCGGGCAAGACAAAT
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FILE REFERENCE: 060193

CURRENT PELLING TOWNER: US/09/601,478

CURRENT FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: JP H10-134679

PRIOR PILING DATE: 1998-03-05

PRIOR FILING DATE: 1998-03-05

PRIOR PILING DATE: 1998-03-05

PRIOR RELING DATE: 1998-02-03

PRIOR FILING DATE: 1998-02-03

**NUMBER OF SEO ID NOS: 11

SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTATTAATGGTGTATTAAAAGTTGTTGTACTTTG
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                                                840;
                                                Length
              ; OTHER INFORMATION: human embryonic brain cDNA library
US-09-601-478-6
                                                Score 838.4; DB 4;
Pred. No. 2.9e-210;
                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 81, Application US/09484970B
Patent No. 6426186
                                               77.68;
99.98;
                                                                    Conservative
sapiens
                                               Query Match
Best Local Similarity
Matches 839; Conserv
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-09-484-970B-81
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us-09-513-365a-2.rni

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ATAAGACTATGCAATAATTTTTAATCATTAGTATTAATGGTGTATTAAAAGTTGTTGTAC 1050
                                                                                                             265 CTACGAAAATATAAGAAAGAAGATGATTTAAACCAGAAGAAACGTCTACAGCAGCTTCT 324
                                                           AAGGGTTATTTGTCTTTTATATATTCGTTTGCTTTCAGAAAATGTTTTAGGGTAAATGC
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                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling TITLE OF INVENTION: Pathway
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300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JAN-1998
15-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09006783A Patent No. 6297366 GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NO. 6297366nan, Revin E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 9
                                                                                                                                                                                                                                                                          APPLICANT: Gudkov, Andrey V
APPLICANT: Garkavstev, Igor
APPLICANT: Riabowol, Karl
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59.0%;
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Best Local Similarity
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STREET: 300
TTW: Chicago
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US-09-006-783A-4
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                                                                                                                                                                                                                                                                                                                 Length 1154;
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6426186 197886.1CB1
LOCATION: 17-37
                                                                                                                                                                                                                                                                                                              Score 825.2; DB 4;
Pred. No. 1e-206;
0; Mismatches 18;
APPLICANT: Jones, Karen A.

APPLICANT: Wolkmuth, Wayne

APPLICANT: Walker, Michael G.

TITLE OF INVENTION: BONE REMODELING GENES

FILE REFERENCE: PB-0014 US

CURRENT APPLICATION NUMBER: US/09/484,970B

CURRENT FILING DATE: 2000-01-18

NUMBER OF SEG ID NOS: 172

SEG ID NO 81

LENGTH.
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ilarity 97.9%;
Conservative
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                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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les 836; Conserv
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US-09-484-970B-81
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                                                                                       385 AATGCTCGAATTGGTGGAAAATCGGGCAAGACAAATGGAGTTACACTCACAGTGTTTCCA 444
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                                     CCAGAGAGCACTAATTAATAGTCAAGAATTGGGAGATGAAAAAATACAGATTGTTACACA
                                                                                                                                                                                              AAGCAAAGATGGATTCCAGCCAACCAGAAAGATCTTCAAGAAGACCCCGCAG--GCAGCG
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CITY: Alexandria STATE: Virginia COUNTRY: United States
ZIP: 2213-1404
COMPUTER READABLE FORM: MEDIUM TYPE: ISLOPY disk
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOCFWARE: Patentin Release #1.0, Version #1.30
CURREWT APPLICATION NUMBER: US/09/258,257
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: GARKAVTSEV, IGOR
APPLICANT: RIABOWOL, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING A TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09258257
Patent No. 5965398
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US-09-258-257-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1902;
                                                                                                                                                                                                                                                                                                                                                 Score 183.8; DB 2;
Pred. No. 1.4e-38;
0; Mismatches 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACAAAAGTACTGAAAAGACAAAAAAGGATAG 897
                                                  US 08/569,721
                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                 17.0%;
57.0%;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 Query Match 17.0°
Best Local Similarity 57.0°
Matches 394; Conservative
                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                      CDS
109..738
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COCATION:

US-09-258-257-1
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509 TCTTCAAGAA--GACCCCGCAGGCAGCGGACCAGTGAAAGCCGTGATTTATGTCACATGG 566
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                                                                         335 CCAACAGCAAGCGCTCACGGCGGCAGCGCAACAACGAGAACGGTGAGAACGCGTCCAGCA 394
                                                                                                                                  395 ACCACGACCACGACGACGACGCCTCGGGCACCCAAGGAGAAGAAGAAGAAGAAGAAGAAGACCTCCA
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                                                                                                                                                                                   627 AGAAAAAGGTTCCAAGGCCAAGCAGGAAAGGGAAGCTTCACCTGTTGAGTTTGCAA
                                                                                                             567 CAAATGGGATTGAAGACTGTGATGATCAGCCACCTAAAGAAAAGAAATCCAAGTCAGCAA
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APPLICATION NUMBER: US/08/569.7712

FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08569721A

Patent No. 6037121

GENERAL INFORMATION:
APPLICANT: RARBOWOL, Karl

TITLE OF INVENTION: DNA SEQUENCE ENCODING A TUI
TITLE OF INVENTION: SUPPRESSOR GENE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathls
STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       867 ACAAAAGTACTGAAAAGACAAAAAAGGATAG 897
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FILING DATE: 08-DEC-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mooi, Leslie A.
REGISTATION UNDRER: 37,047
REFERENCE/DOCKET NUMBER: 028722-128
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (650) 854-7400
TELEFAX: (650) 854-8275
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Virginia
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                        APPLICANT: Garkavtsev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE ING1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns; Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267;
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595 ACAAAGCCCTGGAGAAATCCAAAAAAGAGAG 725
                                                                                                                                                                                                                                                     ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 17.0%; Score 183.8;
| 57.0%; Pred. No. 1.4
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                                                                                      Sequence 1, Application US/09258371
Patent No. 5986078
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: MOO1, LESLIE A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 026
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1902 base pairs
                                                                                                                                                                                                                                                                                                                                        ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
109..741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                          STATE: Vi
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                                                                    US-09-258-371-1
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Best Local S
Matches 394
                                                      RESULT 6
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335 CCAACAGCAAGCGCTCCACGGCGCACCAACAACGAGAACCGTGGAGAACGCGTCCAGCA 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGATGAAAAAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 GCGACGAGAAGATCCAGATCGTGAGCCAGATGGTGGAGCTGGTGGAGAACCGCACGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 AGGTGGACAGCCACGTGGAGCTGTTCGAGGCGCAGCAGGAGCTGGGCGACACAGTGGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     275 ACAGCGGCAAGGTTGGCGCGGACAGGCCCAATGGCGATGCGGTAGCGCAGTCTGACAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             509 TCTTCAAGAA - - GACCCCGCAGGCAGCGGACCAGTGAAAGCCGTGATTTATGTCACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              627 AGAAAAAGAACGCTCCAAGGCCAAGCAGGAAAGGGAAGCTTCACCTGTTGAGTTTGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                  PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 183.8; DB 3;
Pred. No. 1.4e-38;
0; Mismatches 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAATGGAGTTACACTCACAGTGTTTCCAAGATC-----
                                                                                                                                                                                                               NAME: MOOI, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, '
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,230
FILING DATE: .15-NOV-1996
                                                                                                                                CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                 TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 17.0%;
Best Local Similarity 57.0%;
Matches 394; Conservative
                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1902 base pairs
                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
   COMPUTER READABLE FORM:
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109..741
                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: CDNA
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; LOCATION:
US-08-751-230-1
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Patent No. 6117633
GENERAL INFORMATION:
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DUPRESSOR GENE ING1
TITLE OF INVENTION: DUPRESSOR GENE ING1
CORRESPONDENCE ADDRESS:
ADDRESSED: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
                                               Score 183.8; DB 3
Pred. No. 1.4e-38;
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US-08-569-721A-1
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                                                   Query Match
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Patent No. 6238918
GENERAL INFORMATION:
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE
TITLE OF INVENTION: SUPPRESSOR GENE ING1
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
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APPLICATION NUMBER: US/09/258,372
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
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CLASSIFICATION:
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US-09-258-372-1
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APPLICANT: Helbing, Caren C.
APPLICANT: Riabowol, Karl
APPLICANT: Johnston, Randall N.
APPLICANT: Garkavtsev, Igor
TITLE OF INVENTION: METHODS OF MODULATING APPLICS
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                      695 ACAAAGCCCTGGAGAAATCCAAAAAAGAGAG 725
                                                                                        867 acaaaagtac†gaaaagacaaaaaggatag 897
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Pred. No. 1.4
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APPLICATION NUMBER: US/08/828,158
FILING DATE: 27-MAR-1997
APPLICATION NUMBER: US 08/751230
FILING DATE: 15-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
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COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
TYPE: Floppy disk
PC compatible
TYPE: IBM PC COMPATIBLE
PC-DOS/MS-DY
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-854-7400
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illarity 57.0%;
Conservative
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LENGTH: 1902 base pairs
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Patent No. 6143522
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0; Mismatches 267; Indels
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                                         028722-144
ATTORNEY/AGENT INFORMATION:
NAME: MOOL, LEGBIGA.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 0287
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEPHONE: 415-854-7275
                                                                          INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1902 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                   17.0%;
57.0%;
                                                                                                                                                                                                                                                                   Best Local Similarity 57.03
Matches 394; Conservative
                                                                                                                                                                                                 CDS
109..741
                                                                                                                                                            linear
                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                               ; NAME/KEY:
; LOCATION:
US-09-258-372-1
                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,371
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Pred. No. 1.4e-38;
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                                                                    APPLICANT: Garkartsev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODIN
TITLE OF INVENTION: SUPPRESSOR GENE INGI
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: 08/751,230
                  Sequence 9, Application US/09258371
Patent No. 5986078
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NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
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TELECOMMUNICATION INFORMATION
TELEPHONE: 415-854-7400
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57.0%;
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LENGTH: 2061 base pairs
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Best Local Similarity 57.08
Matches 394; Conservative
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STRANDEDNESS: double
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                                                        GENERAL INFORMATION:
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; LOCATION:
US-09-258-371-9
JS-09-258-371-9
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APPLICANT: Riabowol, Karl
APPLICANT: Gandall N.
APPLICANT: Garkavtsev, Igor
TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                              Score 183.8; DB 3;
Pred. No. 1.4e-38;
0; Mismatches 267;
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STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
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Patent No. 6143522
                                              Query Match 17.0%;
Best Local Similarity 57.0%;
Matches 394; Conservative
; LOCATION: 16..900
US-08-751-230-9
                                              Query Match
Best Local Similarity
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US-09-499-082-9
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APPLICANT: Garkavtsev, Igor
APPLICANT: Ralabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE INGI
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/751,230
FILING DATE: US/08/751,230
CLASSIFICATION: 514
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APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTONEY/AGENT INFORMATION:
RAME: MOOI, Leslie A.
REGISTRATION NUMBER: 37,047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/08751230 Patent No. 6117633
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TELECOMMUNICATION INFORMATION
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EDNESS: double
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687 TAGATCCTAATGAACCTACATACTGCTTATGCAACCAAGTGTCTTATGGGGAGATGATAG 746
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                                   674 TCGACCCCAACGAACCCACGTACTGTCTGTGCAACCAGGTCTCCTATGGGGAGATGATCG
                                                                     747 GATGTGACAATGAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTGTTTCACTTACCT
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APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE ING1
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 17.0%; Score 183.8; DB 4; Best Local Similarity 57.0%; Pred. No. 1.4e-38; Matches 394; Conservative 0; Mismatches 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                               867 ACAAAAGTACTGAAAAAGAAAAAGGATAG 897
                                                                                                                                                                                                                                                 854 ACAAAGCCCTGGAGAAATCCAAAAAAAGAGAG 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Mooi, Leslie A.
REGISTATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-144
TELECOMMUNICATION INFORMATION:
TELEPRONE: 415-884-7400
TELEFAX: 415-884-8275
INFORMATION FOR SEQ ID NO: 9:
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APPLICATION NUMBER: US/09/258,372
FILING DATE:
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APPLICATION NUMBER: 08/751,230
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STRANDEDNESS: double
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16..900
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Best Local Similarity
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; LOCATION:
US-09-258-372-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 183.8; DB 3; Length 3
Pred. No. 1.4e-38;
0; Mismatches 267; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAATGGAGTTACACTCACAGTGTTTCCAAGATC------
                                                                                    Patentin Release #1.0, Version #1.30
                                                                                                                                                                      PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/828,158
FILING DATE: 27-MAR-1997
APPLICATION NUMBER: US 08/751230
FILING DATE: 15-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: MOOJ, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-148
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/499,082
             COMPUTER READABLE FORM:
BEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.08;
57.08;
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nucleic acid
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Best Local Similarity 57.03
Matches 394; Conservative
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                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY:
; LOCATION:
US-09-499-082-9
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Search completed: June 20, 2003, 02:42:11 Job time: 85 secs
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US-09-006-783A-2
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                                                                                                                                                                                                                                                                                                                                                                                       TCTTCAAGAA; -GACCCCGCAGGCAGCGGACCAGTGAAAGCCGTGATTTATGTCACATGG. 566
                                                          374 AGGIGGACAGCACGIGGAGCIGITCGAGGCGCAGCAGGAGCIGGGCGACACAGIGGGCA
                                                                                                                                        -CTGCTGAAAGTGAACGAGCCTCAGATAAAGCAAAGATGGATTCCAGCCAACCAGAAAGA
                                                                                                                                                              434 ACAGCGGCAAGGTTGGCGCGGACAGGCCCAATGGCGATGCGGTAGCGCAGTCTGACAAGC
                                                                                                                                                                                                 CAAATGGGATTGAAGACTGTGATGATCAGCCACCTAAAGAAAAGAAATCCAAGTCAGCAA
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                                             GAGATGAAAAATTACAGATTGTTACACAAATGCTCGAATTGGTGGAAAAATCGGGCAAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a Mediator of p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: Gudkov, Andrey V
APPLICANT: Gutkov, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: p33/ING1 as a Mediator of p53
TITLE OF INVENTION: Pathway
NUMBER OF SEQUENCES: 7
NUMBER OF SEQUENCES: ADDRESSE: ADDRESSEE: MCDONNELL Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACAAAGCCCTGGAGAAATCCAAAAAAGAGAG 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACAAAAGTACTGAAAAGACAAAAAAGGATAG 897
                                                                                           AAATGGAGTTACACTCACAGTGTTTCCAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/006,783A
FILING DATE: 15-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09006783A
Patent No. 6297366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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STATE: Illinois
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US-09-006-783A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAGATCCTAATGAACCTACATACTGCTTATGCAACCAAGTGTCTTATGGGGAGATGATAG
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                                                                                                                                                                                                                                                                                                                                                                                          567 CAAATGGGATTGAAGACTGTGATGATCAGCCACCTAAAGAAAAGAAATCCAAGCAA
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                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                       30;
                                                                                                                                                                                                                                                                                                                     Length 2061;
                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                     Score 182.2; DB 4;
Pred. No. 3.7e-38;
0; Mismatches 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAATGGAGTTACACTCACAGTGTTTCCAAGATC---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: No. 6297366nan, Kevin E
REGISTRATION NUMBER: 35,303
REPERENCE/DOCKET NUMBER: 97,837
TELECOMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 56.9%;
Matches 393; Conservative
                                                                                                                                      LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                 MOLECULE TYPE: CDNA
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June 20, 2003, 01:22:25; Search time 192 Seconds (without alignments) 8254.278 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                 1042519 segs, 733713590 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                    OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                          IDENTITY NUC
Gapop 10:0 , Gapext 1.0
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/ cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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/ cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
/ cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Published_Applications_NA:*

Database :

SUMMARIES

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Result No.	Score	Query Match	Query Match Length DB	DB	QI	Description
			-	-		
1	1046	6.96	1078	12	US-10-115-899-7	Sequence 7, Appli
7	838.4	77.6	840	12	US-10-115-899-6	Sequence 6, Appli
m	378.4	35.0	421	6	US-09-918-995-37033	Sequence 37033, A
4	237.4	22.0	873	6	US-09-968-653A-4	Sequence 4, Appli
S	183.4	17.0	8487	10	US-09-764-877-3454	Sequence 3454, Ap
9	182.2	16.9	2061	6	US-09-968-653A-2	Sequence 2, Appli
	174.4	16.1	633	6	US-09-968-653A-6	Sequence 6, Appli
œ	91.6	8.5	1864	6	US-10-037-270-435	5
თ	83.6	7.7	451	6	US-09-854-133-146	-
10	83.6	7.7	451	10	US-09-738-973-146	Sequence 146, App
11	9.99	6.2	993	10	US-09-801-368-257	Sequence 257, App
12	62	5.7	813	6	US-09-938-842A-1178	~
13	56.8	5.3	456	σ	US-09-918-995-16047	Sequence 16047, A
c 14	51.6	4.8	393	10	US-09-960-352-4582	Sequence 4582, Ap
c 15	50.8	4.7	361	10	US-09-919-580-114	Sequence 114, App
c .16	49	4.5	593	φ	US-09-871-161-262	Sequence 262, App
c 17	48.8	4.5	277	10	US-09-960-352-12673	Sequence 12673, A
18	48.4	4.5	5520	О	US-10-001-887-43	Sequence 43, Appl
c 19	48	4.4	527	6	US-10-106-698-863	Sequence 863, App

Sequence 90, Appl Sequence 491, App Sequence 708, App Sequence 6976, Ap	Sequence 14521, A Sequence 17521, A Sequence 8, Appli Sequence 1023, Ap	Sequence 1284, Ap Sequence 690, App Sequence 690, App Sequence 690, App Sequence 338, App	529, A 204, A 4584, 18370, 1369,	Sequence 1689, Ap Sequence 1, Appli Sequence 1, Appli Sequence 13111, A Sequence 1, Appli Sequence 1, Appli Sequence 36, App
US-10-239-676-90 US-10-066-543-491 US-09-919-580-708 US-09-960-325-6976 US-10-198-846-5899	US-09-960-352-14521 US-09-918-995-17652 US-09-998-027-8 US-10-066-543-1023	US-10-066-543-1284 US-10-025-380-690 US-09-922-217-690 US-09-833-263-690 US-09-925-300-338	US-09-764-891-529 US-10-239-676-204 US-09-960-352-4584 US-09-918-995-18370 US-10-198-846-1369	US-10-106-698-1689 US-10-263-316-1 US-09-771-404-1 US-09-918-995-13111 US-10-338-691-1 US-10-066-543-396
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ALIGNMENTS

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ULT 1 10-115-899-7 atent No. US20020151025A1 atent No. US20020151025A1 atent No. US20020151025A1 ENERAL INFORMATION: ENERAL INFORMATION: APPLICANT: OSTUKA PHARMACCEUTICAL APPLICANTION: Human TSC403 gene and human INGIL gene FILE REFERENCE: Q60193 APPLICATION NUMBER: US/10/115,899 CURRENT FILING DATE: 2002-04-05 PRIOR FILING DATE: 2000-08-03 PRIOR FILING DATE: 1998-04-28 PRIOR FILING DATE: 1998-04-28 PRIOR FILING DATE: 1998-04-28 PRIOR FILING DATE: 1998-02-03 PRIOR APPLICATION NUMBER: UP H10-134679 PRIOR PRILING DATE: 1998-02-03 PRIOR APPLICATION NUMBER: UP H10-38133 PRIOR APPLICATION: NUMBER CONTINUM NUMBER OF UP NO 7 TYPE: DNA ORGANISM: HOMO SapienS FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FURNISM: (92)(931)	Score 1046; DB 12; Pred. No. 2.3e-245; 0; Mismatches 5;	GCGCCCGCGCCGCTGCATGTGCGCTGCTGGATGCGGAGGCGGCGGCGGCGACGCCGCGGATGCTGATGCGGAGGCGCGCGGCGGCGCGCGC	CGGCAGGATGTTAGGGCAGCAGCAGCAACTGTACTCGTCGGCTGCGCTCCTGACCGG
SULT 1 -10-115-899-7 squence 7, Application US/10115899 Patent No. US20020151025A1 GENERAL INFORMATION: GENERAL INFORMATION: APPLICATION: Human TSC403 gene a FILE REFERENCE: 060193 FILE REFERENCE: 060193 FILE REFERENCE: 060193 FRIOR PILING DATE: 2002-04-05 PRIOR APPLICATION NUMBER: US/10/115,8 CUBRENT FILING DATE: 1998-04-05 PRIOR APPLICATION NUMBER: JP H10-134679 PRIOR APPLICATION NUMBER: JP H10-134679 PRIOR FILING DATE: 1998-03-05 FRIOR FILING DATE: 1998-03-05 FRIOR FILING DATE: 1998-03-05 FRIOR FILING DATE: 1998-03-05 FRIOR FILING DATE: 1998-02-03 NUMBER OF SEQ ID NOS: 11 SOUTWARR: PatentIN Ver. 2.1 SEQ ID NO 7 LENGTH: 1078 TYPE: DNA ORGANISM: HOMO Sapiens FEATURE: OTHER INFORMATION: human embryonic bra NAME/KEY: CDS LOCATION: (92)(931)	0	CATGTGC CATGTGC	CAGCAGO
-899-7 e 7, Application US/101158 No. US20020151025A1 INFORMATION: INFORMATION: INFORMATION: FILL STATE OF LOG 193 THE TILING DATE: 2002-04-05 APPLICATION NUMBER: US/1 THING DATE: 2000-08-03 APPLICATION NUMBER: US/1 THING DATE: 1998-04-28 APPLICATION NUMBER: UP H10 FILLING DATE: 1998-03-03 APPLICATION NUMBER: UP H10 FILLING DATE: 1998-03-05 FILLING DATE: 1998-02-03 INFORMATION NUMBER: UP H10 NO 7 NO 7 NO 7 NO 7 NO 7 NO 7 NE: Patentin Ver: 2.1 NO 7 NE: COS THEORMATION: human embryo KRE: KRE: THORMATION: human embryo KRE: COS TON: (92)(931)	96.9%; 99.5%; ative	CCGGTG	TTAGGG TTAGGG
Application (1) US200201510255 US200201510255 US200201510255 USENDATION: OSTURA PHEMILING DATE: 060193 USCATION NUMBE: USCATION	96.9 ilarity 99. Conservative	0505005	AGGATG
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RESULT 1 US-10-115-899-7 Sequence 7, Application US/101158; Patent No. US/20020151025A1 GENERAL INFORMATION: APPLICATION HUMBD TSC403; FILE REFERENCE: 060193 CURRENT APPLICATION HUMBER: US/16 CURRENT APPLICATION NUMBER: 09/601 PRIOR FILING DATE: 2000-08-03 PRIOR FILING DATE: 1998-04-28 PRIOR FILING DATE: 1998-04-28 PRIOR FILING DATE: 1998-04-28 PRIOR FILING DATE: 1998-03-03 PRIOR FILING DATE: 1998-04-05 PRIOR FILING DATE: 1998-03-03 PRIOR APPLICATION NUMBER: JP H10 PRIOR FILING DATE: 1998-03-03 PRIOR FILING	Query Match Best Local Similarity Matches 1049; Conser	.,	Σ Ψ
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                                                                                                                                                                                                                                         77.6%; Score 838.4; DB 12; 99.9%; Pred. No. 1e-194; iive 0; Mismatches 1;
CURRENT APPLICATION NUMBER: US/10/115,899
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 09/601,478
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 1988-04-28
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-03-05
PRIOR PRIOR FILING DATE: 1998-03-05
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PRIOR PRIOR DATE: 1998-03-05
SPINGR FILING DATE: 1998-03-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity 99.98
Matches 839; Conservative
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LENGTH: 840
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  GGAGCGGAGCCGGCTGCTCACCTGCTACGTGCAGGACTACCTTGAGTGCGTGGAGTCGCT
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Ltd. and human ING1L gene

APPLICANT: Ostuka Pharmaceutical Co., TITLE OF INVENTION: Human TSC403 gene FILE REFERENCE: Q60193

Sequence 6, Application US/10115899 Patent No. US20020151025A1 GENERAL INFORMATION:

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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411/756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 1201-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR PRILIGE DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 37033
LENGTH: 421
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Pred. No. 1.4e-82;
0; Mismatches 26
                                                                                                            Sequence 37033, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
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; OTHER INFORMATION: D = A,T,C or G
US-09-918-995-37033
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Garkavstev, Igor
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93.8%;
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 CTCGCTGATGCGGGAGATCGACGCGAAATACCAAGAGATCCTGAAGGAGCTAGACGAGTG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       385 AATGCTCGAATTGGTGGAAAATCGGGCAAGACAAATGGAGTTACACTCACAGTGTTTCCA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   288 GATGGTGGAGCTGGTGGAGAACCGCACGCGCAGGTGGACAGCCACGTGGAGCTGTTCGA 347
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TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling Pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 873;
                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff STREET: 300 South Wacker Drive CITY: Chicago
                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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Pred. No. 6.2e-48;
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CLASSIFICATION: CLASSIFICATION: CLASSIFICATION DATA:
APPLICATION NUMBER: US/09/006,783A
FILING DATE: 15-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/968,653A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: NO. USZO0300730073064Anan, Kv
REFISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 97,837
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SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
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59.0%;
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Matches 462; Conservative
                                                       SEQUENCES:
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COUNTRY: USA
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                                                                                                  715 ATGCAACCAAGTGTCTTATGGGGAGATGATAGGATGTGACAATGAACAGTGTCCAATTGA 774
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                             GACCAGTGAAAGCCGTGATTTATGTCACATGGCAAATGGGATTGAAGACTGTGATGATCA 594
                                                                                                                                                                                                                                                                                 708 GIGGIICCACIICICGIGCGIGGGGCICAAICAIAAACCCAAGGGCAAGIGGIACIGICC 767
                                                                                  ----CTGCTGAAAGTGAACGAGCCTCAGATAAAGCAAAGATGGATTCCAGCCAACCAGA
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Patent No. US20020147140A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCOO5

CURRENT FILING DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper

NUMBER OF SEQ ID NOS: 4031

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3454

LENGTH: 8487
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Pred. No. 4e-34;
0; Mismatches 266; Indels
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Best Local Similarity 57.0%;
Matches 395; Conservative
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US-09-764-877-3454
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  505 AAGATCTTCAAGAAGACCCCGCAGGCAGCGGACCAGTGAAAGCCGTGATTTATGTCACAT
                                                                                                                                                                                                              625 AAAGAAAAGAAACGCTCCAAGGCCAAGCGGAAAGGGAAGCTTCACCTGTTGAGTTTGC
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                                                                                                        565 GGCAAATGGGATTGAAGACTGTGATGATCAGCCACCTAAAGAAAAGAAATCCAAGTCAGC
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Riabowol: Karl
TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling
Pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5888 GGACAAAGCCCTGGAGAAATCCAAAAAAGAGAG 6920
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APPLICATION NUMBER: US/09/006,783A
FILING DATE: 15-JAN-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION UNMERS: US/09/968,653A
FILING DATE: 01-Oct-2001
CLASSIFICATION: <UNKnown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 300 South Wacker Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09968653A Publication No. US20030073084A1 GENERAL INFORMATION: GAPPLICANT: Gudkov, Andrey V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
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LENGTH: 2061 base pairs
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STRANDEDNESS: single
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Query Match
Best Local Simi
Matches 250;
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                                                                                                                                                                                                                                                                                                        -CTGCTGAAAGTGAACGAGCCTCAGATAAAGCAAAGATGGATTCCAGCCAACCAGAAAGA
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                                                                                                      Gaps
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                                                                                                     30;
                                                                             Length 2061;
                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: p33/ING1 as a Mediator of Pathway
                                                                             DB 9;
                                                                                                    0; Mismatches 268;
                                                                            Query Match
Best Local Similarity 56.9%; Pred. No. 3.2e-34.
Matches 393; Conservative 0; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACAAAGCCCTGGAGAAATCCAAAAAAGAGAG 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACAAAAGTACTGAAAAGACAAAAAAGGATAG 897
                                                                                                                                                                                                                                                              AAATGGAGTTACACTCACAGTGTTTCCAAGATC-
                    NAME/KEY: CDS
LOCATION: 16..897
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-968-653A-6; Sequence 6, Application US/09968653A; Publication No. US20030073084A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gudkov, Andrey V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Garkavstev, Igor
Riabowol, Karl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                 CDS
16.
 CDNA
MOLECULE TYPE:
FEATURE:
                                                      US-09-968-653A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   522 CCCGCAGCCAGCGGACCAGTGAAAGCCGTGATTTATGTCACATGGCAAATGGGATTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 CACGGCGGCAGCGCAACAACGAGCAGCGTGAGAACGCGTCCAGCAACCACGACCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACGGCGCCTCGGGCACACCCAAGGAGAAGGCCAAGACCTCCAAGAAGAAGAAGCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTGTCCAATTGAATGGTTTCACTTTTCATGTGTTTCACTTACCTATAAACCAAAGGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTIGCCCCATCGAGTIGCTTCCCACTTCTCGTGGGGCTCAATCATAAACCCAAGGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 633;
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                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 174.4; DB 9;
Pred. No. 1.2e-32;
0; Mismatches 126;
                                                                                                                                                                                                                                                                                                                      FILING DATE: 15-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: NO. US20030073084Alnan, Kevin
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 97,837
                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/968,653A
FILING DATE: 01-Oct.-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/006,783A
Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: US-09-968-653A-6
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US-10-037-270-435
; Sequence 435, Application US/10037270
South Wacker
                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION TELEPHONE: 312-913-0001
                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 633 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.1%;
66.5%;
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                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 1..630
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AATCCAAAAAAGAGAG
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                CITY: Chicago
                                                        COUNTRY: USA
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169 CGTGGAGTCGCTGCCCCACGACATGCAGAGGAACGTGTCTGTGCTGCGAGAGCTGGACA 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 GGACCTGGGCGACGAGAAGATCCAGATCGTGAGCCAGATGGTGGAGCTGGTGGAGAACCG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 CGTGGAGTCGCTGCCCCACGACATGCAGAACGTGTCTGTGTGCGGAGAGCTGGACAA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349 AGAATTGGGGAGATGAAAAAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.475C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         409 GGCAAGACAAATGGAGTTACACTCACAGTGTTTCCAAG 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  255 CACGCGGCAGGTGGACAGCCACGTGGAGCTGTTCGAGG 292
                                                                                                                                                                                                                 Score 83.6; DB 9;
Pred. No. 1.5e-10;
0; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.7%; Score 83.6; DB 10; Best Local Similarity 58.6%; Pred. No. 1.5e-10; Matches 163; Conservative 0; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/738,973
CURRENT FILMS DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 587
SOFTWARE: FASTSEQ for Windows Version 3.0
    CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 146, Application US/09738973
Patent No. US20020110563A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reed, Steven G.
Henderson, Robert A.
Lodes, Michael J.
Fling, Steven P.
Mohamath, Raodoh
                                                                                                                                                                                                                   7.7%;
58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mannion, Jane
Kalos, Michael D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Algate, Paul A.
APPLICANT: Secrist, Heather
APPLICANT: Indirias, Carol Marghicant: Benson, Darin R.
APPLICANT: Elliot, Mark
                                                                                                                                                                                                                   Query Match 7.7
Best Local Similarity 58.6
Matches 163; Conservative
                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-854-133-146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapien
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                                                                                         SEQ ID NO 146
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APPLICANT:
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                                                                                                               LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               734 GGGGAGATGATAGGATGTGACAATGAACAGTGTCCAATTGAATGGTTTCACTTTTCATGT 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GITTCACTTACCTATAAACCAAAGGGGAAATGGTATTGCCCAAAGTGCAGGGGAGATAAT 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              674 GTTGAGTTTGCAATAGATCCTAATGAACCTACATACTGCTTATGCAACCAAGTGTCTTAT
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TITLE OF INVENTION: No. US20030104529Alel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 78 4C172B
CURRENT APPLICATION NUMBER: US/10/037,270
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: pt_Flegenes Version 1.0
SOFTWARE: pt_Flegenes Version 1.0
FUND 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Raodoh
APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
FILLE REFERENCE: 210121.475C10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 91.6; DB 9; Length 1:
Pred. No. 4.1e-12;
0; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1394 AAGAGAAGAGCAGCAGACACAAATAAAGG 1423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 146, Application US/09854133
Publication No. US20020183499A1
GENERAL INFORMATION:
No. US20030104529A1
NRMATION:
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64.8%;
                                                                                                                                                                                                                                                                                                                                                                 Tillinghast, John
                                                                                                                       Ren, Feiyan
Chen, Rui-hong
Zhao, Qing A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 64.8<sup>†</sup>
Matches 136<sup>†</sup>, Conservative
                                                                                                                                                                                                                                  Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
                                                                                                                                                                       Zhao, Qing A.
Wehrman, Tom
Xue, Aidong J.
                                                                                                                                                                                                                                                                                             Ma, Yunqing
Wang, Dunrui
Wang, Zhiwei
                                           APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: (164)..(1420)
US-10-037-270-435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-854-133-146
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Indels

Length 451;

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Indels

Length 451;

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APPLICANT: Zhu, TONG
TITLE OF INVENTION: SAME, AND METHODS OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPL300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR PLICATION NUMBER: US 60/300,111
PRIOR PLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-01-65
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR PLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-01-16
PRIOR PLICATION NUMBER: US 60/300,111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    729 CITATGGGGAGATGATAGGATGTGACAATGAACAGTGTC---CAATTGAATGGTTTCACT 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 GGACTACCTTGAGTGCGTGGAGTCGCTGCCCCACGACATGCAGAGAACGTGTCTGTGCT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 GNCCCCATTGTCGNACCCCTAGTCCGTGTGGTGGAATTCGGCGACCGCCATGTACTTGGA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                669 CACCTGTTGAGTTTGCAATAGATCCTAATGAACCTACATACTGCTTATGCAACCAAGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            786 TITCALGITICACITACCIATAAACCAAAGGGGAAAIGGIAITG 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     662 ATACATGCGTTGGCCTCACACCTGAGACCAGATTCAAAGGGAAATG 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROW VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 174;
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Pred. No. 0.00053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 62; DB 9;
Pred. No. 4.1e-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US/09/235,076 PRIOR FILING DATE: 1999-01.20 NUMBER OF SEQ ID NOS: 38054 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16047, Application US/09918995 Publication No. US20030073623A1 GENERAL INFORMATION:
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OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.3%;
Best Local Similarity 49.4%;
Matches 179; Conservative (
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Matches 108; Conservative
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                                              Wang, Xun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-918-995-16047
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APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 GAAATACCAAGAGATCCTGAAGGAGCTAGACGAGTGCTACGAGCGCTTCAGTCGCGAGAC 135
                                                                                                                698 GAACCTACATACTGCTTATGCAACCAAGTGTCTTATGGGGAGATGATAGGATGTGACAAT 757
                                                                                     289 IGATITTAAACCAGAAGAAACGICTACAGCAGCTTCTCCAGAGAGCACTAATTAATAGTCA
                                                                                                                                                                            349 AGAATTGGGAGATGAAAAAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAAATCG
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Pred. No. 3.5e-06;
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CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
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US-09-938-842A-1178
Sequence 1178, Application US/09938842A
Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 257, Application US/09801368 Patent No. US20020128250A1
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SEQ ID NO 257
LENGTH: 993
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ilarity 66.2%;
Conservative
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APPLICANT: Busby, Robert
APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
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Salama, Sofie
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NUMBER OF SEQ ID NOS: 440
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Best Local Similarity
Matches 96; Conserv
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Search completed: June 20, 2003, 02:45:35 Job time: 195 secs
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385 AATGCTCGAATTGGTGGAAAATCGGGCAAGACAAATGGAGTTACACTCACAGTGTTTCCA 444
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                                                                                                                                                                                 127 GCGAGAGCTGGACCAGGAGGAGGAAGATAAGAAAGCAGGATTGACATCCTGGCTGCAGA 186
                                                                                                                                                                                                                                                             274 ATATAA-----GAAAGAAGATGATTTAAACCAGAAGAAGGTCTACAGCGCTTCT 324
                                                                                                                                                                                                                                                                                                                                                                                                             CCAGAGAGCACTAATTAATAGTCAAGAATTGGGAGATGAAAAAATACAGATTGTTACACA 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 ccagaaceccracaecaagrecaaggaaracagreaceacaagrecaecreeccareca 306
                                                                                                                                                                                                                                                                                                                                 187 GTACATCTCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGAT
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Pred. No. 0.0089;
0; Mismatches 114; Indels 0
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) OTHER INFORMATION: Clone ID: 20-LIB3057-013-Q1-K1-E7
US-09-960-352-4582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
TITLE OF INVENTION: WUSCLE ACID AND OTHER MOLECU:
TITLE OF INVENTION: WUSCLE AND EAT DEPOSITION
TITLE OF INVENTION OF SECTION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4582, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
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Best Local Similarity 51.3%;
Matches 120; Conservative
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AG 368
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APPLICANT: Pyle, Ruth

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0
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APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.552
CURRENT APPLICATION NUMBER: US/09/919,580
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 934
SOFTWARE: RastSEQ for Windows Version 4.0
SEQ ID NO 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                           ; NAME/KEY: misc_feature
; CCATION: 49, 89, 101, 141, 209, 253, 305, 324, 331, 360
; OTHER INFORMATION: n = A,T,C or G
US-09-919-580-114
                                                                                                                                                                                                                                                                                                                                                                                                                4.7%; Score 50.8; DB 10;
64.6%; Pred. No. 0.013;
Live 0; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 64.6<sup>5</sup>
Matches 73, Conservative
                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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7 680.8 63.0 919 12 BG211544 8 671.8 62.2 675 14 BM682789 9 663 61.4 664 14 BM719460 10 636.4 58.9 653 13 B1495873 11 632.2 58.5 891 13 B1495873 13 599 55.5 679 10 AV647947 14 553.4 52.2 579 10 AV647947 15 550.8 51.0 703 13 B1546580 16 550.8 51.0 703 13 B1546580 17 547 50.6 547 9 A1186701 18 538.2 49.8 566 12 BE839460 19 537.8 49.8 565 12 BF114684	C 20 528 48.9 552 9 AIR00614 AIR00614 AIR00614 AIR132612.X 21 521 48.2 537 9 AIR57321 AIR57399 AIR57394 GIT12104 AIR5734 GIT12104 AIR5734	452.8 41.9 466 9 AII26389 447.2 41.4 531 9 AA204672 446.6 41.4 531 9 BA204672 440.6 40.8 514 13 BI132471 438.4 40.6 460 10 AW674790 431.8 4 40.0 520 13 BI67689 429.2 39.7 472 12 BE773058 429.3 39.7 587 14 BQ746746 428 39.6 440 12 BF732230 425 39.4 466 12 BF732979	·	AUTHORS Carninci,P. and Hayashizaki,Y. TITLE High-efficiency full-length cDNA cloning JOURNAL Meth. Enzymol. 303, 19-44 (1999) MEDLINE 9927953 PUBMED 10349636 REFRENCE 2 AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itch,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. TITLE Normalization and subtraction of cap-trapper-selected cDNAs to caprepare full-length cDNA libraries for rapid discovery of new genes JOURNAL Genome Res. 10 (10), 1617-1630 (2000) MEDLINE 20499374 PUBMED 11042159
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: June 20, 2003, 01:20:25; search time 1533 Seconds (without alignments) 11409.736 Million cell updates/sec Title: US-09-513-365A-2 Perfect score: 1080 Sequence: 1 qcqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqq	able: IDENTITY NUC Gapop 10.0, Gapext 1.0 16154066 seqs, 8097743376 residues ber of hits satisfying chosen parameters: 32308132 B seq length: 0 B seq length: 200000000 essing: Minimum Match 08 Maximum Match 1008 Listing first 45 summaries	Database : EST:* 1: em_estba:* 2: em_esthum:* 3: em_estin:* 4: em_estin:* 5: em_estro:* 6: em_estpl:* 7: em_estro:* 8: em_htc:* 10: qb_est1:* 11: qb_est2:* 11: qb_est3:* 13: qb_est4:* 14: qb_est4:* 15: em_estfun:*	lestom: * gas.hum: * gas_lnv: * gas_lnv	\$ derived by analysis of the total score distribution. SUMMARIES Query Auch

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                                           with XhoI and SstI. Cloning sites,
                                                                                      Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                         similar to P33ING2"
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88.0%;
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Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Leboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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I (bases 1 to 912)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Onpublished (1999)

L Ontact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.inh.gov

Tissue Procurement: NCI

CONTact: Preparation: Michael Brownstein Laboratory

CDNA Library Preparation: Michael Brownstein Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LCM2058 row: h column: 10

High quality; sequence stop: 587.

Location/Qualifiers

I (1912)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           912 bp mRNA linear EST 07-MAY-2002
AGENCOURT_6738254 NIH_MGC_127 Home sapiens cDNA clone IMAGE:5810745
5', mRNA sequence.
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536
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DEFINITION
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AUTHORS
TITLE
JOURNAL
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KEYWORDS
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prepared from a pool of 40 cell line polyA+ RNAs (bladder -2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -4%, connective tissue -1.4%, eye -1%, intestine -2.6%, kidnney -2.2%, liver -5.7%, lung -10.8%, NK-cell -5.2%, ovary -4%, pharynx -2.5%, prostate -4.3%, salivary 9land -1.3%, and skin -2.3%) 5' and 3' adaptors were used in cloning as follows:
                                                                                                                                     5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and 5'-ATTCTAGAGGCGGCGCGACATG-dT(30)NN-3'. Full-length enriched library was constructed using the Clontech creator SMATR tin a size-selected to contain the 1-2 kb size fraction (other fractions present in NIH_MGC_126 and NIH_MGC_128). Library created in the laboratory of T. Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCTCAGATAAAGGAAGGATGGATTCCAGCCAACCAGAAAGATCTTCAAGAAGACCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCTCAGATAAAGCAAAGATGGATTCCAGCCAACCAGAAAGATCTTCAAGAAGACCCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TACTGCTTATGCAACCAAGTGTCTTATGGGGAGATGATAGGATGTGACAATGAACAGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCGCTCCTGACCGGGGAGCGGAGCCGGCTGCTCACCTGCTACGTGCAGGACTACCTTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCGTGGAGTCGCTGCCCCACGACATGCAGAGGAACGTGTCTGTGCTGCGAGAGCTGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u> AGGCAGCGGACCAGTGAAAGCCGTGATTTATGTCACATGGCAAATGGGATTGAAGACTGT</u>
                                                                                                                                                                                                                                                                                                                                                                             Gaps
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е
                                                                                                                                                                                                                                                                                                                    Score 747.8; DB 14; Length Pred. No. 2.5e-104;
                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                235 g
                                                                                                                                                                                                                                                                                                                                      Query Match 69.2%;
Best Local Similarity 96.9%;
Matches 794; Conservative
                                                                                                                                                                                                                                                                   Library."
184 c
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Gaps

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397

517 556 577

457

376

697

637

316 817 256

757

196

937

877

136

825

g ò BM982877/c DEFINITION

LOCUS

SOURCE

JOURNAL MEDLINE

AUTHORS TITLE REFERENCE

ACCESSION VERSION KEYWORDS

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998 TATGCAATAATTTTTAATCATTAGTATTAATGGTGTATTAAAAGTTGTTGTACTTTGAAA 1057
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 78)
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,C.J., Danzig,J. and Ducar,M.
                                                                                                                                                                                                                                                                                                                                         938 ATTTGTCTTTTATATAATTCGTTTGCTTTCAGAAAATGTTTTAGGGTAAATGCATAAGAC 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG184056 798 bp mRNA linear EST 21-APR-;
RST2972 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
BG184056 GI:13705743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTAATAGTCAAGAATTGGGAGATGAAAAATACAGATTGTTACACAAATGCTCGAATTG
                                                                                                                                                                                                                                                 315 GAACAGTGTCCAATTGAATGGTTTTCACTTTTCATGTGTTTTCACTTACCTATAAACCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      878 GAAAAGACAAAAAGGATAGAAGATCGAGGTAGTAAAGGCCATCCACATTTTAAAGGGTT
                                                                                          735 ATTAATAGTCAAGAATTGGGAGATGAAAAATACAGATTGTTACACAAATGCTCGAATTG
                                                                                                                                                         AGACCCCGCAGGCAGCGGACCAGTGAAAGCCGTGATTTATGTCACATGGCAAATGGGATT
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                                                                                                                                      GTGGAAAATCGGGCAAGACAAATGGAGTTACACTCACAGTGTTTCCAAGATCCTGCTGAA
                                                                                                                                                                                                                               AGTGAACGAGCCTCAGATAAAGCAAAGATGGATTCCAGCCAACCAGAAAGATCTTCAAGA
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    Mismatches
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    Conservative
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    Matches 735;
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AUTHORS
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/lab_host="DH10B (life Technologies) (T1 phage resistant)"
/lab_host="DH10B (life Technologies) (T1 phage resistant)"
/note="Corgan: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EooR I; Site_2: Not I;
U.CF-ENN is a normalized cDNA library containing the following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an ollyo-dT primer containing a Not I site. Double stranded CDNA was ligated on EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The ollyonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dTy18 tail. The sequence tag for this library is CTGCTCAGGT.
                                                                                                                                                                                                   BM982877 11-MAR-2002 UI-CF-EN1 Homo sapiens cDNA clone UI-CF-EN1-acs-d-05-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total John Library of Iowa Med Labs, Iowa City, IA 52242, USA Tel: 319 356 4866
Fax: 319 356 4866
Fax: 319 356 7171
Famil: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAG_LIB=UI-CF-EN1
TAG_TISSUE-Human Lung Epithelial Cell Lines untreated LPS
6hr to LPS 24h
720 CCAATTGAATGGGTTCACTTTTTCATGTGGTTCACTTACCTATAAACCCAAAGGGGAAAT 779
                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 735)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue_type="Primary Lung Cystic Fibrosis Epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 735;
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Pred. No. 2.4e-102;
                                                                   GGTATTGCCCAAAGTGCAGGGGAGATAATGAGAAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="UI-CF-EN1-acs-d-05-0-UI"
/clone_lib="UI-CF-EN1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAG_SEQ-CTGCTCAGGT"
161 c 114 q
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BM982877.1 GI:19606826
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100.0%;
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Contact: McCray, PB
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McCray Lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                discovery
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                                                                                                                                                                                                                                                                                                                                         human.
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FEATURES

EST 21-APR-2001

BASE COUNT ORIGIN

15

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/tissue_type="small cell carcinoma"
/cell_line="McG3"
/lab_host="bill0" (phage-resistant)"
/note="Corgan: lung; Vector: poTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dr priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average.
Insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
california, Berkeley) using ZAP-cDNA synthesis kit
(Siratagene) and Superscript II RT (Life Technologies)."
17 c 230 g 146 t
                                                                                                                                                                                                                                                                       BE796780 793 bp mRNA linear EST 20-SEP-2000 601587557F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941655 5',
                                                                        GGGTAAATGCATAAGACTATGCAATAATTTTAATCATTAGTATTAATGGTGTATTAAAA 1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAGCGGAGCCGGCTGCTACCTGCTACGTGCAGGACTACCTTGAGTGCGTGGAGTCGCT 180
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 793)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nct.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM794 row: a column: 16
                  134 CCACATTTTAAAGGGTTATTGTCTTTTATATATATTCGTTTGCTTTCAGAAAATGTTTTA
                                                                                         61 CGCCAGGATGTTAGGGCAGCAGCAGCAGCAACTGTACTCGTCGGCTGCGCTCCTGACCGG
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Pred. No. 1e-98;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .793
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="laxon:941655"
/clone=lib="NIH_MGC_7"
                                                                                                                                                                                                                                                                     793 bp
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Location/Qualifiers
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Best Local Similarity
Matches 747; Conserv
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                                                                                                                                                                                                                                             /clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression,
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261 ATGTCTACGAAAATATAAGAAAGAAGATGATTTAAACCAGAAGAAACGTCTACAGCAGC 320
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                                                                  Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 12;
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0; Mismatches 4;
                  Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
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                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                          High quality sequence stop: 531.
Location/Qualifiers
   expression
                                                   Contact: Scott J. Cain
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98.98;
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Email: cgapbs-rémail.ini.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

cDNA Library Preparation: Michael J. Brownstein (LLNL)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAMI1661 row: n column: 13

High quality sequence stop: 775.

Inccation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       778 bp mRNA linear EST 05-SEP-2001 603191255F1 NIH_MGC_95 Homo sapiens cDNA clone IMACE:5262540 5', B1548536 B1548536.1 G1:15435848 EST.
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1 (bases 1 to 778)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                       TGAAAAAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCAAGACAAAT
                                                                                                                                                                                    CTAAAGAAAAGCCCAAGTCAGCAAAGAAAAAGAAACGCTCCAAGGCCAAGCAGGAAA
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                                                                       GGAGTTACACTCACAGTGTTTCCAAGATCCTGCTGAAAGTGAACGAGCCTCAGATAAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
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AUTHORS
TITLE
JOURNAL
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/organism="Homo sapiens"

/db xref="taxon:9606"

/clone="IMAGE:526240"

/clone=lib="NIH_MGC.95"

/tissue_type="hippocampus"

/lab_host="bull08"

/note="Organ: brain: Vector: pBluescriptR (modified pBluescript Ks+); Site_l: BamH; Site_2: Sall-XhoI (gtcgag pBluescript Ks+); Site_l: BamH; Site_2: Sall-XhoI (gtcgag pBluescript Ks+); Site_l: BamH; Site_2: Sall-XhoI (gtcgag pBluescript Rs+); Site_l: BamH; Site_2: Sall-XhoI (gtcgag pBluescript Cs+); Site_l: BamH; Site_2: Sall-XhoI (gtcgag pBluescript Rs+); Site_1: BamH; Site_2: Sall-XhoI (gtcgag pBluescript BamH; Site_2: Sall-XhoI (gtcgag                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGCAGGATGTTAGGGCAGCAGCAGCAGCAACTGTACTCGTCGCCTGCGCTCCTGACCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCCCACGACATGCAGAGGAACGTGTCTGTGCTGCGAGAGCTGGACAAAAATATCAAGA
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Pred. No. 3.6e-96;
0; Mismatches 3;
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540

835 900 895 657 955

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TCGTTTGCTTTCAGAAAATGTTTTAGGGTAAATGCATAAGACTATGCAATAATTTTTAAT 1015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: msoares@blue.weeg.ulowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                     Euteleostom1;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 675)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 9250
Fax: 319 335 9565
                   656 GAAAGGGAAGCTTCACCTGTTGAGTTTGCAATAGATCCTAATGAACCTACATACTGCTTA
                                                                                                                                               716 TGCAACCAAGTGTCTTATGGGGAGATGATAGGATGTGACAATGAACAGTGTCCAATTGAA
                                                                                                                                                                                                                    776 IGGITICACTITICATGIGITICACITACCIAIAAACCAAAGGGGAAAIGGIAIIGCCCA
                                                                                                                                                                                                                                                                                             836 AAGTGCAGGGAGATAATGAGAAAACAATGGACAAAAGTACTGAAAAAGACAAAAAGGAT
                                                                                                                                                                                                                                                                                                                               601 NAGTGCAGGGGAGAATATGAGAAAACAAAG--ACAAAGCACTGAAAAGACAAAAAGG-T
                                                                                                                                                                                                                                                                                                                                                                      AGAAGATCGAGGTAGTAAAGGCCATCCACATTTTAAAAGGGTTATTTGTCTTTTATATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="fetal eyes, lens, eye anterior segment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ытовы/ву 11-estl-ajf-g-22-0-UI.sl UI-E-EJl Homo sapiens cDNA clone UI-E-EJl-ajf-g-22-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 818
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Program for Rat Gene Discovery and Mapping
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/clone="UT-E-E11-aif-g-22-0-UI"
/clone_lib="UI-E-EJ1"
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Seq primer: Ml3 Forward
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                                                                      BG211544 919 bp mRNA linear EST 21-APR-2001
RST31111 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
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1 (bases I to 919)

Rarrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Velsoo, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher Creation of genome-wide protein expression libraries using random activation of gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is H11080, since a random activation method was used, these sequence tags are not necessarily expressed in H11080 under normal circumstances."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAATGGAGTTACACTCACAGTGTTTCCAAGATCCTGCTGAAAGTGAACGAGCCTCAGAT
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Pred. No. 3.5e-94;
0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       Athersys, Inc.
3201 carnegie Ave, Cleveland, OH 44115, USA
TTE1: 216 431|9900
Fax: 216 361|9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
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21227151
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                                                                    919 bp
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: scain@athersys.com
                                                                                                                          BG211544.1 GI:13733231
                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.0%;
95.1%;
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les 788; Conservative
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EST 01-MAR-2002

Euteleostomi;

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according to Bonaldo. Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dr primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAMCCAAGA; eye anterior segment, AATGCCGCAT; optic nerve, CCATTAAGTG; retina, CGCGG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Towa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
7e1: 319 335 8250
Fax: 319 335 8256
Email: msoares@lue.weeg.ulowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seg primer: M13 Reverse.
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//dev_stage="fetal and adult"
//lab host="DH10B (Life Technologies) (T1 phage resistant)"
//note="Corgan: eye; Vector: pT713-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-EJ1 is a subtracted cDNA library constructed
  75 TATGCAATAATTTTTAATCATTAGTATTAATGGTGTATTAAAAGTTGTTGTACTTTGAAA 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches to facilitate gene
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/db_xref="taxon:9606"
/clone="UI-B-EJI-ajf-g-22-0-UI"
/clone="Lib="UI-B-EJI"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
                                                                                                                                                                                      664 bp mRNA linear EST 01-UI-E-EJI-ajf-g-22-0-UI.rl UI-E-EJI Homo sapiens cDNA clone BM719460.1 GI:19038113
EST
                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 664)
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Matches 663; Conservative
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                                 /dev_stage="fetal and adult"
//lab_host="DH10B (Life Technologies) (TI phage resistant)".
//lab_host="DH10B (Life Technologies) (TI phage resistant)".
//note="Organ: eye; Vector: pTT7=pec (Pharmacia) with a modified polylinker; Site_1: EDCN I; Site_2: Not I;
UI-E-EJ1 is a subtracted CDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-df primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I; and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tall. The sequence tags for this library are: fetal eyes, AGNATCAAGA; lens, CGATTAGCGA; eye anterior segment, AATGCCGCAT; optic nerve, CCATTAAGT; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Chorold, ACCTAA. This library was created for the program, Gene Discovery in the Visual mach return in the Visual mach in the interpretation is the interpretation in the visual mach in the visual mach in the visual mach in the visual mach interpretation is a contained by National Eye Institute (NEI).
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B1495873 | GI:15325***
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Departments of Pathology and
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/clone_lib="Morton Fetal Cochlea"
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/dev_stage="16-22 week fetus"
/dev_stage="16-22
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                                                                                                                                                         National Institutes
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                                                                                                          Email: ccmorton@lics.bwh.harvard.edu

DNA sequencing and analyses were performed by National Institut

of Health Intramural Sequencing Center (NISC; see

http://www.nisc.uhh.gov).

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@lmage.llnl.gov) for further information.

Plate: LLAM6327 row: G column: 7
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       Harvard Medical School, Boston, MA
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Pred. No. 2.3e-87;
); Mismatches 1; I
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99.8%;
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75 Francis Street,
Tel: 617 732 7980
Fax: 617 738 6996
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BI460319 708 bp mRNA 11near EST 21-AUG-2001
603201967F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5267729 5',
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
TobNa Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
TobNa Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 708)
NIH-MGC http://mgc.ncl.nih.gov/.
Mational Institutes of Health, Mammallan Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                               753 ACAATGAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTGTTTCACTTACCTATAAAC
                                                                                                                                       813 CAAAGGGGAAATGGTATTGCCCAAAGTGCAGGGGAGATAATGAGAAAAACAATGGACAAAA
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Plate: LLAM1675 row: f column: 18
High quality sequence stop: 700.
Location/qualifiers
1. 708
//organism="Homo sapiens"
//db_xref="taxon:9606"
//clone=lib="MAGE:5267729"
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BI460319
BI460319.1 GI:15250975
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BI091047.1 GI:14509377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      633 AGAAACGCTCCAAGGCCAAGCAGGAAAGGGAAGCTTCACCTGTTGAGTTTGCAATAGATC 692
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NHI-NGC http://mgc.nol.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.e. column: 10
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              DB 13;
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96.5%; Pred. No. 8.2e-87;
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/db_xref="taxon:9606"
/clone="IMAGE:4996593"
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/cell_line="MGC36"
/lab_host="DH108"
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Location/Qualiflers
1. .891
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BI091047/c
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KEYWORDS
SOURCE
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TITLE
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1. 679
/ Organism="Homo sapiens"
/ Organism="Homo sapiens"
/ db xref="taxon:9606"
/ clone="GLCBDD03"
/ clone="GLCBDD03"
/ tissue_type="corresponding non cancerous liver tissue"
/ dev_stage="Adult"
/ lab_host="SOLR"
            Pudong, Shanghai
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                                                                                                                                                                                                                                                                                 CGGCAGGATGTTAGGGCAGCAGCAGCAGCAACTGTACTCGTCGGCTGCGCTCCTGACCGG
                                                                                                                                                                              /note="Vector: pBluescript sk(-); Site_1:
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                                                                                                                                                                                                                                    Length
Genome Center at Shanghai
Zhangjiang Hi-Tech Park,
                                                                   in Shanghai
                                                                                                                                                                                                                                                         22;
                                                                                                                                                                                                                                   Score 599; DB 10;
Pred. No. 1e-81;
); Mismatches 22;
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          351 Guo Shouling Road, Zhangjiang 201203, P. R. China Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Fmail: hanzqehgc.sh.cn
This clone is available at CHGC in Location/Qualifiers
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I (bases 1 to 679)

S Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,O., Cal,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Z., Cheng,Z., Li,N., Du,J., Hu,M., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.

Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver with those of corresponding noncancerous liver (at.)

L Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

Contact: Zeguang Han
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 679 bp mRNA linear EST 15-JAN-2002 GLC Homo sapiens cDNA clone GLCBDD03 3', mRNA sequence.
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                                                                  GTTAGGGCAGCAGCAGCAGCAGTGTACTCGTCGGCTGCGCTCCTGACCGGGGAGCGGAG
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                      Score 607; DB 13;
Pred. No. 6.1e-83;
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National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Other_ESTS: ba59f06.y1

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: ATC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNI at:

image.llnl.gov/image/html/iresources.shtml

Seq primer: -40UP from Gibco

High quality sequence stop: 420.

Location/Qualifiers

Location/Qualifiers
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                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DaS9f06.xl NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900867 3' similar to TR:095698 095698 ING1LP. ;, mRNA sequence. AW674008
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Pred. No. 2.8e-76;
0; Mismatches 7; Indels 0;
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_10"
/cell_line="MGC36"
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Best Local Similarity 98.8%;
Matches 567; Conservative
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Tel: +55-11-2704922
Fax: +55-11-2707001
Email: sainpsondludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2=RC3-FN0143-190 700-022-dl2&t3-2000-07-19&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 564.

I. 564
/organism="Homo sapiens"
/db_xref="taxon:9606"
/dev_atage="Adult"
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Sagres,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                AGAAAATGTTTTAGGGTAAATGCATAAGACTATGCAATAATTTTTAATCATTAGTATTAA 1027
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
Gaps
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llarity 99.5%; Pred. No. 7e-75;
Conservative 0; Mismatches 3;
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/product= "Tumour suppressor homologue protein, p33ING2"
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8244.604 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                             The present sequence is a DNA encoding tumour suppressor homologue protein, p331NG2 which is homologous to human tumour suppressor protein, p471NG3. The tumour suppressors of the invention are involved in the regulation of cell proliferation and in the control of cellular aging, anchorage dependence and apoptosis. The tumour suppressor protein, p471NG3, nucleic acids encoding it and antibodies against it are useful for diagnosis, prevention and treatment of tumours and cancers. The p471NG3 DNA is also used in gene therapy.
                       New tumor suppressor protein p471NG3 for the diagnosis and treatment of
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                                                                                                                                                             Best_Local Similarity 100.0%;
Matches 1080; Conservative C
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                                                                                                                                                      721 CCAAGTGTCTTATGGGGAGATGATAGGATGTGACAATGAACAGTGTCCAATTGAATGGTT
                                                                                                                                    CAGGGGAGATAATGAGAAAACAATGGACAAAAGTACTGAAAAAGACAAAAAGGATAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; TSC403; ING1L; diagnosis; lung cancer; cell cycle; regulation;
cell proliferation; cell aging; apoptosis; tumour suppressor; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents the human tumour suppressor gene INGIL. The present invention also describes the human gene TSC403 expressed specifically in normal lung tissue. TSC403 is useful in the diagnosis, investigation and treatment of cancers in which it is overexpressed, including cancer of the lung, breast, fallopian tube, oesophagus, colon, thyroid, parotid gland, bladder, ovary or pancreas. INGIL is useful in the investigation of cell proliferation, aging and apoptosis and the pathology of cancer, the diagnosis and treatment of cancer such as cancer of the colon, stomach, oesophagus or fallopian
                                                                                                                                                                                                                                                                                                                                                                                                                                                       cycle; regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; TSC403; ING1L; diagnosis; lung cancer; cell cycle; regulat
proliferation; cell aging; apoptosis; tumour suppressor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tube, and the screening of candidate drugs for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer tissue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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Pred. No. 1.7e-181;
); Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human lung-specific gene TSC430 overexpressed in for treatment of, e.g. colon tumour
                                                                                          given"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 14; Page 91; 99pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "ING1L"
                                                                                                                                                                                                                                                               BP.
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98JP-0038133.
98JP-0073234.
                                                                                                                                                                                                                                                               AAZ08595 standard; cDNA; 840
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ilarity 99.9%;
Conservative
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                                                                                                           CGTCTACAGCAGCTCTCCCAGAGAGCACTAATTAATAGTCAAGAATTGGGAGATGAAAAA
                                                                                                                                         ATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCAAGACAAATGGAGTTA
                                                                                                                                                                        CACTCACAGTGTTTCCAAGATCCTGCTGAAAGTGAACGAGCCTCAGATAAAGCAAAGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  suppressor (TUSUP) nucleotide sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ47473 standard; cDNA; 1153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human
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Tumour suppressor protein; TUSUP; human; cancer; treat; prevent; reproductive tract; gastrointestinal tract; immune system; ss.
                                                                                                               Location/Qualifiers
277..999
/*tag= a
                                                                                                 Homo sapiens
                                                                                                                Key
RESULT 4
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AAAGAAACGCTCCAAGGCCAAGCAGGAAGGGAAGCTTCACCTGTTGAGTTTGCAATAGA 690

631

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TUSOP sequence was identified from a human lung cDNA library. The protein is 240 amino acids in length and has one potential CAMP and CGMP dependent protein kinase phosphorylation site, nine potential protein kinase c phosphorylation site, five potential casein kinase phosphorylation sites, five potential casein kinase phosphorylation sites, five potential casein kinase phosphorylation sites, five potential tyrosine kinase phosphorylation sites, and one potential tyrosine kinase phosphorylation site. Tusor has structural and chemical similarity to p33. Tusopp can be used to treat or prevent cancer, particularly of the reproductive or gastrointestinal tracts or of the immune system. Agonists of the Tusop protein can be used to raise Tusop specific antibodies and to screen for specific binding agents and potential therapeutic agents. The Tusop diagnostic probes and primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence encodes the human tumour suppressor (TUSUP) protein. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                             particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAATATAAGAAAGAAGATTTAAACCAGAAGAAACGTCTACAGCAGCTTCTCCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 GCTGCGAGAGCTGGACAACAATATCAAGAAACGTTAAAGGAAATTGATGATGTCTACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human tunmour suppressor protein for treating cancer, Ereproductive and gastrointestinal tracts or immune system
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                          suppressor protein"
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                                                                                                                                                                                                                                                                                                                                Patterson C;
/product= TUSUP
/note= "Tumour :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; Fig 1; 71pp; English.
                                                                                                                                                                         99WO-US11136
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                                                                                                                                                                                                                                                                                 (INCY-) INCYTE PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-062711/05.
P-PSDB; AAY52199.
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ID AA247474 standard;
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Matches 343;
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                                                                                                                                                                                                                                                                                                                                                                                                       sequence tag; secreted protein; cDNA isolation; mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because, they are often obtained from oligo-dT primed cONA libraries. Such ESTs are not well suited for isolating cDNA sequences
                            TGACAATGAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTGTTTCACTTACATAA
                                                                  ACCAAAGGGGAAATGGTATTGCCCAAAGTGCAGGGGAGATAATGAGAAAACAATGGACAA
                                                                                                         AAGTACTGAAAAGACAAAAAGGATAGAAGATCGAGGTAGTAAAGGCCATCCACATTTTA
                                                                                                                                                                           AAGGGTTATTTGTCTTTTATATATTCGTTTGCTTTCAGAAAATGTTTTAGGGTAAATGC
                   TCCTAATGAACCTACATACTGCTTATGCAACCAAGTGTCTTATGGGGAGATGATAGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                    secreted protein 5' EST, SEQ ID NO: 32534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID 32534; 71pp + CD-ROM; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy; chromosome mapping;
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derived from the 5' ends of mRNAs and even in those cases where longer both Sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 ATTGATGATGTCTACGAAAAATATAAGAAAGAAGATGATTTAAACCAGAAGAAACGTCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 AGCCAACCAGAAAGATCTTCAAGAAGACCCCGCAGGCAGCGGACCAGTGAAAGCCGTGAT
                                                                                                                                                                                                                                                                                                                                                                            ATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCAAGACAAATGGAGTTACACTCA
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                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  suppressor protein; TUSUP; human; cancer; treat; prevent;
                                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                               346;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human tumour suppressor (TUSUP) fragment nucleotide sequence.
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                                                                                                                                                                                                                                               DB 21; Length
                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                               Sequence 346 BP; 130 A; 63 C; 80 G; 70 T; 3 other;
                                                                                                                                                                                                                                             Score 332.2; DB 2
Pred. No. 3.2e-66;
                                                                                                                                                                                                                                                                                                1; Mismatches
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970 AAAATGTTTTAGGGTAAATGCATAAGACTATGCAATAATTTTTAATCATTAGTATTAATG 1029
            suppressor protein (TGSUP) see AAY52199. The TGSUP protein is 240 mino acids in length and has one potential CAMP and CGMP dependent protein kinase phosphorylation site, nine potential protein kinase phosphorylation site, five potential casein kinase phosphorylation site, five potential casein kinase phosphorylation site, site, and one potential tyrosine kinase phosphorylation site. TGSUP has structural and chemical similarity to pi3: TGSUP can be used to treat or prevent cancer, particularly of the reproductive or gastrointestinal used to raise TUSUP specific antibodies and to screen for specific binding agents and potential therapeutic agents. The TUSUP nucleotide sequence can be used in gene therapy and as a source of diagnostic probes
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                                                                                                                                                                                                                                                                                                                                                                                                      849
                                                                                                                                                                                                                                                                                                                                                       850 TAATGAGAAAACAATGGACAAAAGTACTGAAAAGACAAAAAAGGATAGAAGATCGAGGTA 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 GTAAAGGCCATCCACATTTTAAAGGGTTATTTGTCTTTTATAATTCGTTTGCTTTCAG 969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 AAAATGTTTAGGGTAAATGCATAAGACTATGCAATAATTTTTAATCATTAGTATTAATG 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    790 ATGTGTTTCACTTACCTATAAACCAAAGGGGAAATGGTATTGCCCCAAAGTGCAGGGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        730 TIATGGGGAGATGATAGGATGTGACAATGAACAGTGTCCCAATTGAATGGTTTCACTTTTC
 This sequence was used to determine the sequence of the human tumour
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   p53; tumour; cancer; detection; antibody; hybridisation; exon 1b; ING1; ing1; p331NG1; p371NG1; oncogene; gene therapy; diagnosis; proliferation disorder; transformation; transformed cell; mouse; ds.
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0
                                                                                                                                                                                                                                                                30.1%; Score 325; DB 21; Length 325; 100.0%; Pred. No. 1.4e-64; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                   Sequence 325 BP; 103 A; 71 C; 36 G; 115 T; 0 other;
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/product= P37ING1 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGTATTAAAAGTTGTTGTACTTTG 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine P37ING1 coding sequence.
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/*tag= a
                                                                                                                                                                                                                                                                                                   Matches 325; Conservative
                                                                                                                                                                                                                                                                                   Similarity
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1039 ACCCAGAAAGGGCCGGGTACTGCACTGCATCCAGAGGCCCCTGATCCGCAGCCAGGAGCTA 1098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer etiology. However, along was not a useful gene to study in cancer etiology. However, alternative initiation exons of the ingl gene, each having their own promoter have been discovered. Expression of one promoter (1a) produces a protein identical to ING1. Expression of a second promoter (1b) produces a protein having an identical C-terminal fragment to ING1 but an additional 104 converninal amino acids. The newly discovered protein has been designated p371NG1 (Wild type: p331NG1). p371NG1 has the characteristics of an oncogene. When overexpressed in cells (even those expressing wild type p53) p371NG1 is able to cause those expressing wild type p53) p371NG1 is able to cause proliferation or transformation of those cells. Thus detecting a nucleic acid encoding exon 1b of ing1 by hybridisation with an cultication or transformation of those cells. Thus detecting a nucleic acid having the sequence of exon 1b of ing1 by hybridisation with an or its antisense sequence can identify individuals expressing the oncogenic form of ing1. Novel peptide sequences taken from the 104 con also be used in detection methods for the p371NG1 variant. The polypeptides may be useful in gene therapy for treatment of cell proliferation disorders, especially cancers and for diagnosing and
                                                                                                                                                                                               Detecting nucleic acid encoding exon 1b of ing1, useful for diagnosing and treating cancer, comprises contacting sample with isolated nucleic acid comprising sequence of exon 1b and detecting hybridized products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 TCGCTGCCCCACGACATGCAGAACGTGTCTGTGCTGCGAGAGCTGGACAAATAT
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                                                                                                                                                                                                                                                                                                                                                                                            The P53 pathway occurs in a much larger proportion of tumours. In many cases the mechanism of functional inactivation of the p53 gene instances the mechanism of functional inactivation of the p53 gene instances the mechanism of functional inactivation of the p53 gene instances of more p53 has been found to act in cooperation with ING1. Functional cooperation between ING1 and p53 suggested that ING1. Encoded a tumour suppressor protein that functioned within the p53 pathway. This data suggested a possible role for ING1 in head and neck cancers and chromosomal location of the ING1 placed it within a region that is frequently rearranged in head and neck cancers. Large scale analysis of tumours involving ING1 has not revealed mutations in ING1 nor significant variations in its expression suggesting that ING1 was soft a useful gene to study in
                                                                                                                                                                                                                                                                                                                                               Mutations in or loss of the p53 gene occur in more than 50% of human tumours and tumour cell lines, but functional inactivation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.5%; Score 253.6; DB 21; Length 2817;
11arity 60.3%; Pred. No. 5.7e-48;
Conservative 0; Mismatches 289; Indels 33;
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                                                                         Grigorian IA;
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0; Mismatches
                                                                      Gurova KV,
                                                                                                                                                                                                                                                                                                Disclosure; Fig 11; 134pp; English.
                    UNII ) UNIV ILLINOIS FOUND.
                                                                      Zeremski M,
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                      CAGGTGGACAGTCACGTGGAGCTCTTCGAAGCACCACGGACATCAGTGACGGCACTGGT
                                                   -----GTGAACGAGCCTCAGATAAAGCAAAGATGGATTCCAGCCAACCAGAAAGATCT
                                                                                                          -GACCCCCCAGCAGCGGACCAGTGAAAGCCGTGATTTATGTCACATG
                                                                                                                                                                                         1339 AATCACGACCATGATGACATCACCTCAGGAACGCCCAAGGAGAAAAAGCAAAAAACCTCA
                                                                                                                                                                                                                    AAGAAAAAGAAACGCTCCAAGGCCAAGCAGAAAGGGAAAGCTTCACCTGTTGAGTTTTGCA
                                                                                                                                                                                                                                                                           ATAGATCCTAATGAACCTACATACTGCTTATGCAACCAAGTGTCTTATGGGGAGATGATA
                                                                                                                                                                                                                                                                                                                                GGATGTGACAATGAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTGTTTCACTTACC
                                                                                                                                                               GCAAATGGGATTGAAGACTGTGATGATCAGCCACCTAAAGAAAAGAAATCCAAGTCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   p53; tumour; cancer; detection; antibody; hybridisation; exon 1b; ING1; ing1; p33ING1; p37ING1; oncogene; gene therapy; diagnosis; proliferation disorder; transformation; transformed cell; human;
CAAATGGAGTTACACTCACAGTGTTTCCAAGATCCTGCTGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACAAAAGTACTGAAAAGACAAAAAAGGATAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA53792 standard;
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145 265 476 445 264 205 324 384 325 444 385 534 594 565 654 human tumours and tumour cell lines, but functional inactivation of the p53 pathway occurs in a much larger broportion of tumours. In many cases the mechanism of functional inactivation of tumours. In nany cases the mechanism of functional thactivation of tumours. In remains unknown but p53 has been found to act in cooperation with ING1 encoded a tumour suppressor protein that functioned within the p53 pathway. This data suggested a possible role for ING1 in head and neck cancers and chromosomal location of the ING1 placed it within a region that is frequently rearranged in head and neck cancers. Large scale analysis of tumours involving ING1 has not revealed mutations in ING1 nor significant variations in its cancer etiology. However, alternative initiation exons of the ing1 gene, each having their own promoter have been discovered. Expression of one promoter (la) produces a protein having an identical C-terminal fragment to ING1 but an additional 104 N-terminal anino acids. The newly discovered protein has been classificated p37ING1 (wild type: p33ING1). p37ING1 has the characteristics of an oncogene when overexpressed in cells (even those expressing wild type: p33ING1). p37ING1 has the collect acid encoding exon 1b of ing1 by hybridisation with an isolated nucleic acid having the sequence of exon 1b of ing1 the sequen 266 GCAGCGCGCGCTGATCCGCAGCCAGGAGCTGGGCGACGAGAAGATCCAGATCGTGAGCCA 385 AATGCTCGAATTGGTGGAAAATCGGGCAAGACAAATGGAGTTACACTCACAGTGTTTTCCA -----CTGCTGAAAGTGAACGAGCCTCAGATA GCCCCAGCAGCAGCTGGGCGACACAGGCGCAACAGCGGCAAGGTTGGCGGGAACAGCCC 86 CTATGTGGAGGACTACCTGGACTCCATCGAGTCCCTGCCTTTCGACTTGCAGAAATGT GTCTGTGCTGCGAGAGCTGGACAACAAATATCAAGAAACGTTAAAGGAAATTGATGATGT AAGCAAAGATGGATTCCAGCCAACCAGAAAGATCTTCAAGAAGACCCCGCAG--GCAGCG 446 CAATGGCGATGCGCTAGCGCAGTCTGACAAGCCCCAACAGCAAGCGCTCACGGCGGCAGCG GACCAGTGAAAGCCCGTGATTTATGTCACATGGCAAATGGGATTGAAGACTGTGATGATCA 506 CAACAACGAGAACCGTGAGAACGCGTCCAGCAACCACGACGACGACGGCGCCTCGGG CTACGAAAAATATAAGAAAGAAGATGATTTAAAACCAGAAGAAACGTCTACAGCAGCTTCT 206 CTACGAGCGCTTCAGTCGCGAGACAGACGGGGCGCAGAAGCGGCGGATGCTGCACTGTGT CTACGTGCAGGACTACCTTGAGTGCGTGGAGTCGCTGCCCCACGACGATGCAGAGGAACGT Gaps han 50% of inactivation of or its antisense sequence can identify individuals expressing the oncogenic form of ingl. Novel peptide sequences taken from the 104 Noterninal peptide of p37ING1 can also be used to raise antibodies that can also be used in detection methods for the p37ING1 variant. The polypeptides may be useful in gene therapy for treatment of cel 30; Length Indels Sequence 911 BP; 228 A; 255 C; 305 G; 123 T; 0 other; The polypeptides may be useful in gene therapy for teriferation disorders, especially cancers and for DB 21; Score 237.4; DB 21, Pred No. 1.9e-44; 0; Mismatches 22.0%; 445 AGATC------Conservative Similarity cancers. Matches 462; 265 325 595 studying Query Match Best Local 9 145 477 à g ŏ g à g δ g ò g ò g ò 셤 ö a

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The present sequence encodes a human cancer associated antigen. The sequence is a variant of the ING1 gene, which is a tumour suppressor gene candidate. The cancer associated antigen polynucleotides and polypeptides are useful for screening for the possible presence of a pathological condition in a subject such as cancer. The cancer associated antigen polypeptides are useful for producing vaccines.
                                                                                                                                                                   Sequence 1533 BP; 336 A; 431 C; 521 G; 244 T; 1 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cancer associated antigen; ING1; tumour suppressor; cancer; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer associated nucleic acid molecule identified by SEREX ical identification of antigens by recombinant expression technique, useful in nucleic acid based therapies to treat
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ab5. 867, aa: Asp)"

acancer associated antigen"
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(SLOK ) SLOAN KETTERING INST CANCER RES.
(CORR ) CORNELL RES FOUND INC.
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                                 Gaps
                                32;
 Length 1533;
                                 Indels
 Score 236; DB 22;
Pred. No. 4.7e-44;
0; Mismatches 290;
 21.9%;
58.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention discloses monoclonal antibodies which can be used, in combination, to specifically recognise epitopes of ING1 (inhibitor of growth 1) protein isoforms. ING1 is a tumour suppressor gene and its expression is regulated through the cell cycle, peaking in the S phase. Expression of ING1 is down regulated in breast tumours and lymphoid malignancies. Overexpression of a construct containing the ING1 eners is able to inhibit cell growth by reducing the fraction of cells which enter ing protein in a cell, which involves selecting a cells that ectopically or endogenously expresses ING1 protein. The anti-ING1 monoclonal antibody combination consists of two or more antibodies of CAbi-CAbi0 (not defined), preferably a mixture of CAbi-CAb4, which can detect at least two different isoforms of ING1. The antibodies are also useful for diagnosing a disease e.g. tumour or medical condition in an animal corferably, human) associated with aberrant levels of an ING1 protein. The sequence presented is the human inhibitor of growth 1 (ING1) isoform, protein used to raise antibodies.
                                                                                                                                                               Human; gene; ss; monoclonal antibody; epitope; inhibitor of growth 1;
ING1; tumour suppressor; cell cycle; breast tumour; lymphoid malignancy;
cell growth; anti-ING1; CAb; isoform; diagnosis; tumour; antigen;
p33ING1b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel monoclonal antibody which specifically recognizes epitope of ING1, inhibitor of growth 1 protein, and designated CAb1-10, useful for detecting two different isoforms of ING1 and diagnosing a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 58.9%; Pred. No. 6e-44;
Matches 462; Conservative 0; Mismatches 290; Indels 32
                                                                                                                                     Human inhibitor of growth 1 (ING1) isoform, p33ING1b, cDNA
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873..1712
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ABK86977 standard; cDNA; 2897
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96US-0751230.
95US-0569721.
2000US-0532868.
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BOLAND D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nutations in or loss of the p53 gene occur in more than 50% of human tumours and tumour cell lines, but functional inactivation of human tumours and tumour cell lines, but functional inactivation of tumours. In many cases the mechanism of functional inactivation of the p53 gene remains unknown but p53 has been found to act in cooperation with remains unknown but p53 has been found to act in cooperation with right expectation between ING1 and p53 suggested that ING1. Functional cooperation between ING1 and p53 suggested that ING1. Functional cooperation between ING1 and p53 suggested that ING1 encoded a tumour suppressor protein that functioned within the p53 pathway. This data suggested a possible role for ING1 in head and neck cancers and chromosomal location of the ING1 placed it within a region that is frequently rearranged in head and neck cancers. Large scale analysis of tumours involving ING1 has not within a region that ING1 mas not a useful gene to study in cancer ethology. However, alternative initiation exons of the ing1 expression of one promoter (1a) produces a protein identical canch maying their own promoter have been discovered. Expression of one promoter (1b) produces a protein having ency each maying their own promoter (1b) produces a protein having the network at a second promoter (1b) produces a protein having the network of second promoter (1b) p37ING1 has the designated p37ING1 (wild type ip 331ING1). p37ING1 has the characteristics of an oncogene. When overexpressed in cells (even those expressing wild type p33 p7ING1 is able to cause proliferation or transformation of those cells. Thus detecting a proliferation or transformation of those cells. Thus detecting a solated mucleic acid having the sequence of exon 1b of ing1 or its antisense sequence can identify individuals expressing the concepenic form of ing1. Novel peptide sequences taken from the 104 or that can also be used in detection methods for the p37ING1 wariant. The polypeptides may be useful in gene therapy for treatment of call
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 TGAAGGAGCTGGACGACTACTATGAGAAGTTCAAACGGGAACAGGACGGCACCCAGAAAGC 66
                                                                                                                                                                                                            Detecting nucleic acid encoding exon 1b of ingl, useful for diagnosing and treating cancer, comprises contacting sample with isolated nucleic acid comprising sequence of exon 1b and detecting hybridized products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          306 AACGTCTACAGCAGCTTCTCCAGAGAGCACTAATTAATAGTCAAGAATTGGGAGATGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCAAGACAAATGGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1835 BP; 541 A; 387 C; 468 G; 439 T; 0 other;
                                                                                                                                                 Grigorian IA;
                                                                                                                                                  Gurova KV,
                                                                                                                                                                                                                                                                               Claim 17; Fig 6; 134pp; English.
                                                                                99US-0118941.
                                               04-FEB-2000; 2000WO-US02959
                                                                                                                (UNII ) UNIV ILLINOIS FOUND
                                                                                                                                                  Zeremski M,
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                                                                                                       247 AGGGGGCCAGGACAAGTCGAAGAGTGAGGCCATCACACAGGCAGATAAGCCGAATAACA
                                                                                                                                                            576 TTGAAGACTGTGATGATCAGCCACCTAAAGAAAAGAAATCCAAGTCAGCAAAGAAAAAGA
                                                                                                                                                                                                    367 ATGATGACATCACCTCAGGAACGCCCAAGGAGGAAAAAGCAAAAAACCTCAAAGAAGAAGA
                                                                                                                                                                                                                                                                                                                           ATGAACCTACATACTGCTATGCAACCAAGTGTCTTATGGGGAGATGATAGGATGTGACA
                                                                                                                                                                                                                                                                                                                                                                   487 ACGAGCCCACGTACTGTCTGTGCAACCAGGTCTCCTACGGGGAGATGATCGGCTGTGACA
                                                                                                                                                                                                                                                                                                                                                                                                            ATGAACAGTGTCCCAATTGAATGGTTTCACTTTTCATGTGTTTTCACTTACCTATAAACCAA
                                                                                -----CCCGCAGCCAGCGGACCAGTGAAAGCCGTGATTTATGTCACATGGCAAATGGGA
                                                                                                                                                                                                                                               AACGCTCCAAGGCAAGCAAGGAAAGGCAAGCTTCACCTGTTGAGTTTGCAATAGATCCTA
163 ACGAGCCTCAGATAAAGCAAAGATGGATTCCAGCCAACCAGAAAGATCTTCAAGAAGAC-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide sequence of a human cancer associated antigen.
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/transl_except= "(pos: 25..30, aa: Cys)"
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24-OCT-2000; 2000US-0602362.
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ING1; p33ING1; breast cancer; brain cancer;

(first entry)

Location/Qualifiers 109..741 /*tag= a

sapiens

INC

96WO-CA00819 96US-0751230 95US-0569721

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Tumour suppressor gene ING1 partial cDNA
                                                                                                                                                                                                                                                   (UYTE-) UNIV TECHNOLOGIES INT
                                                              Tumour suppressor gene; ING; diagnosis; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 853
                                                                               The sequence is the wildtype of the ING1 gene, which is a tumour suppressor gene candidate. The cancer associated antigen polynucleotides and polypeptides are useful for screening for the possible presence of a pathological condition in a subject such as cancer. The cancer associated antigen polypeptides are useful for producing vaccines.
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                                                                                                                                                                                                                                                                                                    AGGTGGACAGCCACGTGGAGCTGTTCGAGGCGCAGCAGGAGCTGGGCGACACACTGGGCCA
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cancer associated nucleic acid molecule identified by SERE) leal identification of antigens by recombinant expression technique, useful in nucleic acid based therapies to treat
                                                                                                                                                                DB 22; Length 1143;
                                                                                                                                                                                      30;
                                                                       sequence encodes a human cancer associated antigen
                                                                                                                                                                Score 183.8; DB 22; Length
Pred. No. 3.4e-32;
0; Mismatches 267; Indels
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                                                                                                                                             Sequence 1143 BP; 289 A; 291 C; 366 G; 197 T; 0 other;
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                                                                                     Isolated tumour suppressor gene, ING1 - useful to develop products for inhibiting or increasing cell proliferation, in particular for treatment or diagnosis of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 183.8; DB 18; Length 1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30;
                                                                                                                                                                                                                                                                       A partial cDNA clone (AAT69651), designated ING1, codes for a tumour suppressor protein p331NG1 (AAW19118) that is a potent inhibitor of cell growth. It was isolated by subtractive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 4.1e-32;
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                                                                                                                                                                                                                 Claim 1; Fig 2; 63pp; English
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proliferation of cancer cells.
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Best Local Similarity 57.0%;
Matches 394; Conservative
WPI; 1997-332781/30.
                            P-PSDB; AAW19118
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                      275 ACAGCGCCAAGGTTGGCGCGCGACAGGCCCAATGGCGATGCGGTAGCGCAGTCTGACAAGC 334
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                                               TCTTCAAGAA - - GACCCCGCAGCGCAGCGGACCAGTGAAAGCCGTGATTTATGTCACATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human; apoptosis; cell death; breast cancer;
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P-PSDB; AAW79674.
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This is the nucleotide sequence of a human ING1 (INhibitor of Growth) partial cDNA clone that codes for a pi33ING1 polypeptide (see AAW9674), a novel inhibitor of cell growth and a candidate tumour suppressor. ING1 is a new gene that is expressed in normal mammary epithelial cells, but which is expressed only at lower levels in several cancercus mammary epithelial cell lines and is not expressed in many primary brain tumours. To isolate ING1, a subtractive hybridisation of breast cancer cell line cDNAs was performed with CDNA from normal mammary epithelial cells, and subtracted cDNAs were cloned into retrovirus vector piNCX. Following passage through a packaging line, normal mouse mammary epithelial cells, and subtracted cDNAs were infected, and infected cells were infected into nude mice. Putative transforming fragments from tumours were isolated by PCR (see AAV62290-91) and subcloned into LNCX. An ING1 fragment was obtained and used to screen normal human fibroblast and HeLa cell cDNA libraries. 2 clones were sequenced to obtain the partial ING1 sequence. The complete cDNA sequence (see AAV62292) was obtained by RACE. A claimed method to potentiate apoptosis in a eukaryotic cell involves administering an active pagning method for inhibiting apoptosis in a eukaryotic cell involves administering an active involves administering an active and are an an objective characteristics of a metanotic characteristics of a care a method for inhibiting apoptosis in a eukaryotic cell involves administering an active administering
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Sequence 1902 BP; 574 A; 390 C; 462 G; 476 T; 0 other

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Leotide sequence of a human ING1 (INhibbi con a close that codes for a pl33ING1 por a novel inhibitor of cell growth and a sor. InK1 is a new gene that is expressed that is cells, but which is expressed only a can cercous mammary epithelial cell line in any primary brain tumours. To isolate the primary brain tumours. To isolate the conform organd mammary epithelial cell conversion or and mammary epithelial cell swere cloned into retrovirus vector planes were cloned into the swere cloned into the swere infected, and infected cells were putative transforming fragments from that incomplete conformal human for and used to screen normal human for a sequence of the complete conformal human for an olly sequence and involves administering as or an ollgonuclectide encoding such as an ollgonuclectide encoding such as the derivative cell involves administering as an antisense ollgonuclectide. An an assay for determining the apoptotic characterist in an an antisense ollgonuclectide. An an ansay for determining the allogical activity. The derivatives or variants that may be used derivatives or variants that may be used waryotic cancer cells.	Similarity 57.0%; Score 183.8; DB 19; Length Similarity 57.0%; Pred. No. 4.1e-32; 4; Conservative 0; Mismatches 267; Indels	aagaaacgttaaaggaaattgatgatgtctacgaaaaatataagaagaagatgatttaa 	ACCAGAAGAACGTCTACAGCAGCTTCTCCAGAGAGCACTAATTAAT	GAGATGAAAAAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCAAGAC 	aaatggagttacactcacagtgtttccaagatc	-CTGCTGAAAGTGAACGAGCTCAGATAAAGCAAAGATGGATTCCAGCCAACCAGAAAGA	TCTTCAAGAAGACCCCGCAGGAGCGGACCAGGAAAGCCGTGATTATGTCACATGG 	CAAATGGGATTGAAGACTGTGATGATCAGCCACCTAAAGAAAAGAAATCCAAGTCAGCAA 	agaaaaagaaacgctccaaggccaagcagaaagggaagcttcacctgttgagtttgcaa 	TAGATCCTAATGAACCTACATACTGCTTATGCAAGTGTCTTATGGGGAGATGATAG
This is the nuclea Growth) partial of Growth) partial of tase Any 9644), a tumour suppressor mammary epithelia levels in several not expressed in subtractive hybricacted connactive hybricacted connactive hybricacted or subtracted or subtracted or subtracted or subtracted by PCR (isolated by Antial ING) and PCR (isolated by SinG) peptide of A claimed method for a method for activity in a eukaryotic cell, activity in a eukaryotic cell, activity in a eukaryotic sell, activity in a eukaryotics in eukarapetosis in eukarapeto	Query Match Best Local Sin Matches 394;	237	297	357	417	450	509	567 395	627	687 515
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747 GATGTGACAATGAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTGTTTCACTTACCT 806

INGI nucleic acids can a decreased level of can also be used in gene of cancer cells.

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Sequence 2061 BP; 602.A; 439 C; 515 G; 505 T; 0 other;
                       be used in the diagnosis of breast cancer;
ING1 mRNA indicates cancerous cells. They
therapy methods to block the proliferation
      number of human cancers have been mapped.
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  A full-length cDNA clone (AAT69652), designated ING1, codes for a novel 33 kDa tumour suppressor protein p33ING1 (AAM19119), formerly p33IG1, that is a potent inhibitor of cell growth. A partial clone (AAT69651) was isolated by subtractive hybridisation between normal mammary and transformed epithelial cDNAs, isolation of an antisense ING1 cDNA insert that caused increased cell proliferation, and use of the insert to screen normal human fibroblast and HeLa cDNA libraries. The complete ING1 sequence was then obtd. by 5'RACE. ING1 is localised to the 13q33-34 chromosome region, to which a
                                                                                                                                                                                                                                                                                                                                                                                                                                        gene; ING1; p33ING1; breast cancer; brain cancer;
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/note= "reverse primer 4"
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17.0%; Score 183.8; DB 18; Length 2061; 57.0%; Pred. No. 4.2e-32;
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Nagashima, M., Shiseki, M., Miura, K., Hagiwara, K., Linke, S.P., Pedeux, R., Wang, X. W., Yokota, J., Riabowol, K. and Harris, C.C. DNA damage-inducible gene p331NG2 negatively regulates cell proliferation through acetylation of p53
Eroc. Natl. Acad. Sci. U.S.A. 98 (17), 9671-9676 (2001)
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Submitted (12-MAR-1998) Laboratory of Human National Cancer Institute, 37 Convent Drive Bethesda, MD 20892, USA
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SOURCE
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PRI 18-MAR-1999

AB012853 1078 bp mRNA linear Homo saplens ING1L mRNA for ING1Lp, complete cds. AB012883

RESULT 4
AB012853
LOCUS
DEFINITION
ACCESSION

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/Translation-"MIGOQOQOLYSSAALLTGERSRLLTCYVODYLECVESLPHDMQR
NVVVLRELDNRYQETLKEIDDVYEKYKKEDDLMQKRRLQQLLQRALINSQELGDEKIO
IVTQMLELVENRARQMELLSQCFQDPASSERASDKAKMDSQPERSSRRPRQRTSES
RDLCHMANGIEDCDDOPPKEKSKGAKKKRSRAKQEREASPVEFAIDPNEPYCLCN
OVSYGEMIGCDNEQCPIEWFHFSCVSLLYKPKGKWYCPKCRGDNEKTMDKSTERTKKD
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                                        Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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Shimada,Y., Saito,A. and Horie,M.,
Submission
Submitted (07-APR-1998
Yoshikasu Shimada, Otsuka Pharmaceutical
Co. Ltd., Otsuka GEN Research Institute; Kagasuno, Kawauchi-cho,
Tokushima, Tokushima 771-0192, Japan
(E-mail:shim@otsuka.genome.ad.jp, Tel:81-886-65-2888(ex.2476),
                                                                                              Horie,M.
1, a candidate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAGCGGAGCCGGCTGCTCACCTGCTACGTGCAGGACTACCTTGAGTGCGTGGAGTCGCT
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      to mRNA
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Shimeda,Y., Saito,A., Suzuki,M., Takahashi,E. and Hori
Cloning of a novel gene (INGIL) homologous to ING1, a
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Homo sapiens fetal tissue_lib:fetal-brain cDNA Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebr.
Mammalia; Eutheria; Primates; Catarrhini; Homin
                                                                                                                                                  Cytogenet. Cell Genet. 83 (3-4), 232-235 (1998) 99172097
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99.5%; Pred. No. 6.5e-215;
ive 0; Mismatches 5;
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/dev_stage="fetal"
/tissue_lib="fetal-brain"
1. .1078
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/protein_id="BAA36419.1"
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                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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/chromosome="4"
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Location/Qualifiers
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/product="p32 protein"
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Pred. No. 1.6e-170;
); Mismatches 2;
/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="breast tumor"
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                                         /gene="ing2"
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                       TAAAGAAAAGAAATCCAAGTCAGCAAAGAAAAAAAAGCGCTCCAAGGCCAAGCAGGAAAG
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            TGAAAAAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCAAGACAAAT
                                                    GGAGTTACACTCACAGTGTTTCCAAGATCCTGCTGAAAGTGAACGAGCCTCAGATAAAGC
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Submitted (08-JUN-1998) Lopez-Otin C., Bioquimica y Biologia
Molecular, Universidad de Oviedo. Facultad de Medicina., C/ J
Claveria s/n!, 33066, SPAIN
Location/Qualifiers
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Eukaryota; Métazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
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Cal,S., Freije,J.M. and Lopez-Otin,C.
ING2,a new possible gene supressor tumor
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AJ006851.1 GI:12053587
ing2 gene; p32 protein.
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AC107214 10-APR-2002 Homo sapiens chromosome 4 clone RP11-367N14, WORKING DRAFT SEQUENCE, 8 unordered pieces.
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Catarrhini; Hominidae; Homo.
TTGGGAGATGAAAAAATACAGATTGTTACACAAAATGCTCGAATTGGTGGAAAAATCGGGGCA
                                                                                          237 TTGGGAGATGAAAAAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCA
                                                                                                                                                   653 CAGGAAAGGAAGCTTCACCTGTTGAGTTTGCAATAGATCCTAATGAACCTACATACTGC
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ARG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
Homo sapiens.
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1 (bases 1 to 189972)
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Catarrhin1; Hominidae; Homo.
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Location/Qualifiers
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Mammalla; Eutheria; Primates; Catarrhin1; Hominidae; H
1 (bases 1 to 974)
Nagashima, M., Hagiwara,K., Minter,A.R. and Harris,C.C.
Direct Submission
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//dLxref="taxon:9606"
order(AF062747.1:1. .423,1. .938)
/gene="iNG2"
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Pred. No. 1.2e-165;
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join(AF062747.1:68. .239,124.
/gene="ING2"
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/gene="ING2"
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/gene="ING2"</pre>
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11 Similarity 99.6%;
819; Conservative
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                                                                                Louis,
      Waterston, R. H.
Direct Submission
Submitted (10-APR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. On Apr 10, 2002 this sequence version replaced q1:18677601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: This is a 'working draft' sequence. It currently consists of 8 configs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                   Sequencing vector: plasmid; 100%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator BH; Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 189641 bases at least Q40
Consensus quality: 199699 bases at least Q30
Consensus quality: 199699 bases at least Q20
Insert size: 1204000; agarose-fp
Insert size: 120574; sum-of-contiss
Quality coverage: 11.39 in Q20 bases; sum-of-contiss
Quality coverage: 10.96 in Q20 bases; sum-of-contiss
                                                                                                                                                            Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of unknown length

contig of 1847 bp in length

contig of 1121 bp in length

gap of unknown length

gap of unknown length

contig of 1138 bp in length

gap of unknown length

contig of 1108 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6966: gap of unknown length
37117: contig of 30151 bp in length
37217: gap of unknown length
101402: contig of 64185 bp in length
101502: gap of unknown length
189972: contig of 88470 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1252: contig of 1252 bp in length
                                                                                                                                                                                             //genome.wústl.edu/gsc/index.shtml
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/note="assembly_name:Contig44"
4521. .5658
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1353. :3199
/note="assembly_name:Contig29"
3300. :4420
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/note="assembly_name:Contig65"
37218. .101402

    Summary Statistics

                                                                                                                                             Genome Center
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/db<u>|</u>xref="taxon:9606"
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147244 147365 GATAGAAGATCGAGGTAGTAAAGGCCATCCACATTTTAAAGGGTTATTTGTCTTTTATAT 147424 147064 1012 712 892 412 472 772 832 652 233 TATCAAGAAACGTTAAAGGAAATTGATGATGTCTACGAAAAATATAAGAAGAAGATGAT 413 AGACAAATGGAGTTACACTCACAGTGTTTCCAAGATCCTGCTGAAAGTGAACGAGCCTCA 533 CGGACCAGTGAAAGCCGTGATTTATGTCACATGGCAAATGGGATTGAAGACTGTGATGAT 653 CAGGAAAGGGAAGCTTCACCTGTTGAGTTTGCAATAGATCCTAATGAACCTACATACTGC TTATGCAACCAAGTGTCTTATGGGGAGATGATAGGATGTGACAATGAACAGTGTCCAATT CCAAAGTGCAGGGGAGATAATGAGAAAACAATGGACAAAAGTACTGAAAAAGACAAAAAAG GATAGAAGATCGAGGTAGTAAAGGCCATCCACATTTTAAAGGGTTATTTGTATTTATAT AATTCGTTTCCTTTCAGAAATGTTTTAGGGTAAATGCATAAGACTATGCAATAATTTTT 353 TTGGGAGATGAAAAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCA GAATGGTTTCACTTTTCATGTGTTTCACTTACCTATAAACCAAAGGGGAAATGGTATTGC Gaps Length 189972; ö 147485 AATCATTAGTATTAATGGTGTATTAAAAGTTGTTGTACTTG 147526 700 others Indels AATCATTAGTATTAATGGTGTATTAAAAGTTGTTGTACTTTG 1054 Score 817.2; DB 2; Pred. No. 3.8e-165;); Mismatches 3; 54950 t

540 657 900 717 099 777 720 837 780 897 840 957 868

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658 AAGGGAAGCTTCACCTGTTGAGTTTGCAATAGATCCTAATGAACCTACATACTGCTTATG
                                                                                                                                                                                              601 GAGGGAGGCATCCTGTCGAGTTTGCCATCGATCCCAATGAGCCCACCTACTGCTTGTG
                                                                                                                                                                                                                                                                    718 CAACCAAGTGTCTTATGGGGAGATGATAGGATGTGACAATGAACAGTGTCCAATTGAATG
                                                                                                                                                                                                                                                                                           GTTTCACTTTTCATGTGTTTCACTTACCTATAAACCAAAGGGGAAATGGTATTGCCCAAA
                                                                                                                                                                                                                                                                                                                                                                                     AAGATCGAGGTAGTAAAAGGCCATCCACATTTTAAAGGGTTATTTGTCTTTTATATAATTC
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HTG, HTGS_PHASE1.
Rattus norvegicus.
Rattus norvegicus
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//brotein_id="AAG12173.1"
//db_xref="G1:10039543"
//db_xref="G1:10039543"
//db_xref="G1:10039543"
//db_xref="G1:100"
//d
  ROD 09-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 GTCGAAGATGGATTCCAGTCAACCGGAAAGATCTTCTAGAAGACCTCGAAGACAGAGGAC 480
                                                                                                                                                                                       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1001)
Nagashima,M., Hagiwara,K., Hancock,A.R. and Harris,C.C.
Direct Submission
Submitted (16-JUL-1998) Laboratory of Human Carcinogenesis,
National Cancer Institute, National Institutes of Health, 37
Convent Dr., BldG: 37, RR. 2C01, Bethesda, MD 20892, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGATGAAAAAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGGCAAGACA
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0; Mismatches 111; Indels
mRNA linear complete cds.
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18834 1001 bp
musculus p33ING2 (Ing2) mRNA,
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
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/product="p33ING2"
                                                                   AF078834.1 GI:10039542
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/gene="Ing2"
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al Similarity 88.1%;
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I (Dades I to 10624.)

Muzny,D.W., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barboroks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barboria,J., Benton,J., Binage,K., Blankenburg,R., Bonnin,D., Buck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J. Chavez,D., Chen,Z., Chen,Z., Chowdhry,I., Christopoulos,C., Carlon,Z., Chowlary,I., Christopoulos,C., Davila,M.L., Davis,C., Coyle,M.D., Dathorne,S.R., David,R., Daland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Deland,C.D., Elago,M.D., Dung,Y., Dunh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguco,D., Flagy,N., Ford,J., Foster,P., Frantz,P., Gorrell,J.H., Guevara,W., Ganrer,T., Garza,N., Gill,R., Gao,J., Garcia,A., Garner,T., Garza,N., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hame,S., Hamilton,K., Homes,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Kratsovic,J., Kureshi,A., Leal,B., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Luna,R., Luna,R., Luna,R., Lucier,R., L
AC128348 168245 bp DNA linear HTG 19-JUL-2002 Rattus norvegicus clone CH230-129P3, *** SEQUENCING IN PROGRESS AC128348
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          Massey, E., Mawhiney, E., McLedd, M. P., Maddor, M., Matcher, Morabat, K., Morgan, M., Morris, S., Miner, S., Mickerson, J., Mowtson, M., Nguyen, M., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Okwoon, E., Novéenkwo, S., Oguh, M., Okwoon, G., Morens, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Qitles, M., Ren, Y., Rives, M., Rojas, A., Primus, E., Pu, L. L., Quilles, M., Ren, Y., Scherr, S., Scott, G., Shen, H., Shocshtari, N., Sisson, I., Sodergen, E., Sonaike, T., Sparks, A., Stanley, H., Stonaike, Tansey, J., Taylor, C., Taylor, P., Tamerisa, A., Tamerisa, K., Tang, H., Usman, Y., Vera, Y., Varal, Y., Washington, C., Watlington, C., Warliams, G., Walliams, G., Walliams, G., Walliams, G., Walliams, G., Walliams, C., Walliams
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NOTE: This is a 'working draft' sequence. It currently consists of 50 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as'it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor Polage of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: Plasmid;
Sequencing vector: Plasmid;
Chemisty: Dye-terminator Big Dye: 100% of reads
Assembly; program: Phrap; version 0.990329
Consensus quality: 115858 bases at least Q40
Consensus quality: 122576 bases at least Q30
Consensus quality: 127579 bases at least Q30
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: higs-help@bcm.tmc.edu
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COMMENT

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Homo sapiens
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4 157304: contig of 9011 bp in length
5 157404: gap of unknown length
15 168245: contig of 10841 bp in length
Location/Qualifiers
                                                                                                        Score 686.8; DB 2;
Pred. No. 4.4e-137;
0; Mismatches 77;
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/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="cR330-129P3"
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Best Local Similarity 90.5
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Direct Submitsion
Submitted (15-NAR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
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                                                                                                             Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo
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Center code: WUGSC
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              Homo sapiens chromosome 4 clone R
PROGRESS ***, 26 unordered pieces
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Mammalia; Eutheria; Primates;
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"hote-"assembly_name:Contig56"
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/note-"assembly_name:Contig57"
10470. 11648
11749. 13201
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5163. .6294
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                                                                                                            Length 42029;
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                                                                                                         Score 574.6; DB 2; Length
Pred. No. 4.8e-113;
0; Mismatches 104; Indels
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Best Local Similarity 84.7
Matches 577; Conservative
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                                                                 Wagner, M.J., Gogela-Spehar, M., Skirrow, R.C., Johnston, R.N., Riabowol, K. and Helbing, C.C. Expression of Novel ING Variants Is Regulated by Thyroid Hormone in the Xenopus laevis Tadpole 19. Biol. Chem. 276 (50), 47013-47020 (2001)
                                                                                                                                                                                                                                                                                                                                                                         /product="p321NGL"
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SFGEMIGCDNDECTIEWFHFSCVGLTYKPKGKWYCPDCRGDNEKTMNKNTDKTKKDRR
                                                                                                                                                                                            Direct Submission
Submitted (16-NOV-2000) Biochemistry and Microbiology, University
of Victoria, P.O. Box 3055 Stn. CSC, Victoria, British Columbia V8W
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          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
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Helbing,C.C., Wagner,M.J., Gogela-Spehar,M., Skirrow,R.C.,
Johnston,R.N. and Rlabowol,K.
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Pred. No. 7.4e-83;
0; Mismatches 312;
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                                                                                                                                                                                                                                                                               /organism="Xenopus laevis"
/db_xref="taxon:8355"
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                                                                                                                                                                                                                                                                                                          /tissue_type="brain"
/dev_stage="tadpole"
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Wurdy, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Adioroks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Balbytooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buday, C., Burch, P., Burkett, C., Burchl, K.L., Byrd, N.C., Carroh, T.F., Carter, M., Cavazcos, S.R., Chacko, J., Chavez, D., Carroh, T.C., Coyle, M.D., Dathorne, S.R., David, R., David, M.H.H., David, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Dublin, K.J., Earnhart, C., Edgar, D., Edareth, D., Edareth, D., Edareth, P., Earnhart, C., Edgar, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gorrell, J. H., Guevara, W., Ganner, T., Garzs, N., Hart, M., Havlak, P., Hale, S., Hamilton, K., Hartis, C., Hartis, K., Hart, M., Havlak, P., Hale, S., Hamilton, K., Homsi, F., Howard, S., Huber, J., Hulby, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jiayet, S., Yovar, C., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., 188087 bp DNA linear HTG 31-JUL-2002 Rattus norvegicus clone CH230-6112, *** SEQUENCING IN PROGRESS ***, 69 unordered pieces. 978 979 TAGGGTAAATGCATAAGACTATGCAATAATTTTTAATCATTAGTATTAATGGTGTATTAA 1038 992 TAAAGAAACTGTTTTAGATACAATGTGATATTTTAATAGTACTGAAATATTAAAACCTTT 1051 678 828 918 653 713 738 833 893 953 GATGATAGGATGTGACAATGAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTTTC 798 534 ATCTGAAAGGTCTACACGTAGGCCTCGCAGACAGCGCAATAGTGAGAGCCACGACTTGTG GTCAGCAAAGAAAAGAAACGCTCCAAGGCCAAGCAGGAAAGGGAAGCTTCACCTGTTGA 919 ATCCACATITTAAAGGGTTATTTGTCTTTTATAATTCGTTTGCTTTCAGAAAATGTTT TCACATGGCAAATGGGATTGAAGACTGTGATGATCAGCCACCTAAAGAAAAGAAATCCAA GTTTGCAATAGATCCTAATGAACCTACATACTGCTTATGCAACCAAGTGTCTTATGGGGA ACTTACCTACAAACCAAAGGGCAAATGGTATTGTCCTGACTGCAGAGGACAATGAAAA AACAATGGACAAAAGTACTGAAAAGACAAAAAAGGATAGAAGGTCGAGGTAGTAAAGGCC ACTTACCTATAAACCAAAGGGGAAATGGTATTGCCCAAAGTGCAGGGGAGATAATGAGAA Norway rat. Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost: Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

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Kratovic,J. Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lui,X., Ludier,R., Luda,R., May,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M., Moser,M., Mei,C., Metzker,M., Moser,M., Moser,M., Moser,M., Moser,M., Moser,M., Moser,M., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuon,G., Oragunye,N., Oviedo,R., Parce,A., Payton,B., Peery,J., Perez,L., Pickers,R., Primus,E., Pu,L.L., Oulles,M., Ran,Y., Rives,M., Rojas,A., Primus,E., Pu,L.L., Oulles,M., Ran,Y., Scherer,S., Scott,G., Shen,H., Shochtari,N., Sisson,I., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Tansey,J., Taylor,C., Taylor,P., Tanlera,A., Tamerisa,R., Tang,H., Tansey,J., Taylor,C., Taylor,P., Tanley,M., Thomas,N., Thomas,N., Tusney,S., Ward-Moore,S., Warther,R., Washington,C., Watlilams,G., Walliams,G., Walliams,G., Walliams,G., Walliams,G., Walliams,G., Walliams,G., Walliams,G., Washington,C., Walliang,G., Walliams,G., Mulliams,G., Malliams,G., Malliams,G.
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NOTE: This is a 'working draft' sequence. It currently consists of 69 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Worley, K.C.
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COMMENT

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protein
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                                                       /product="p33ING1 proteir
/protein_id="AAF09183.1"
/db_xref="G1:6456562"
                    /organism="Mus musculus'
                              /db_xref="taxon:10090
Location/Qualiflers
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                                                 /codon_start=1
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Best Local Similarity 60.6
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Mammalla; Eutherla; Rodentla; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 840)
Rancourt, D. and Garkavtsev, I.
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Submitted (11-MAY-1999) Genome Therapeutics Corp., 100
Waltham, MA 02453, USA
                                                                unknown length
of 2585 bp in length
unknown length
of 2418 bp in length
                                                                                                                                                                                                                             Pred. No. 4.4e-48;
Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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bp in length
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of 3045 bp in length
unknown length
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of 2408 bp in 1
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of 3235 l
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of 3267
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/translation-"MLSPANGEQIHLVNYVEDYLDSIESLPFDLQRNYSLMREIDAKY
QEILKELDDYYEKFRRETDGTQKRRVLHCIQRALIRSQELGDEKIQIVSQMVELVENR
SRQVDSHVELFEAHQDISDGTGGSGKAGQDKSKSEAITQADKPNNKRSRRQRNNENRE
                                                            NASNNHDHDD ITSGTPKEKKAKTSKKKRRSKAKAEREASPADFPIDPNEPTYCLOMOY
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                                                                                                                                                                                                                                                                             116 ACCGGGGAGCGGAGCCGGCTGCTCACCTGCTACGTGCAGGACTACCTTGAGTGCGTGGAG
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Pred. No. 5.5e-45;
0; Mismatches 287;
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AF177757 2817 bp mRNA linear ROD 12-DEC-1999
Mus musculus ING1 protein (Ing1) mRNA, alternatively spliced,
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Zeremski,M., Hill,J.E., Kwek,S.S., Grigorian,I.A., Gurova,K.V., Garkavtsev,I.V., Diatchenko,L., Koonin,E.V. and Gudkov,A.V. Structure and regulation of the mouse ingl gene. Three alternative
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116 ACCGGGGAGCGGAGCCGGCTGCTCACCTGCTACGTGCAGGACTACCTTGAGTGCGTGGAG 175
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                      416 CAAATGGAGTTACACTCACAGTGTTTCCAAGATCCTGCTGAAA-----
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Oblikelddyyekrrrethostokrrylhcioralirsobledberioivsonyenr
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Nasnnhidholispyrekrakatskkrrskakaberaspadleidenefyslicuoy
Sygemigcondecpiewphfscyglunikpkgkwycpkcressektmokalekskkera
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months old, gross tissue." /clone_lib="NCI_CGAP_Mam5" /lab_host="DH108"
                                                                                                                                         BC016573 How musculus, inhibitor of growth family, member 1, clone MGC:27881 IMAGE:349601, mRNA, complete cds.
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1584)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X., Hulyk, S.W., Hale, S.M., S., Martin, R.G., Muzny, D.M.,
                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (31-CCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapb2-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amgebcm.tmc.edu
Gunaratne, P.H., Garcla, A.M., Lu, X., Huly'
Yoon, V.S., Kowis, C.R., Lawrence, S., Mark
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
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                           897
                                              793 GACAAAGCCCTTGAGAAGTCCAAGAAAGAGAG 824
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                             GACAAAAGTACTGAAAAGACAAAAAAGGATAG
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NASNNHDHDDITSGTPKEKKAKTSKKKRRSKAKAEREASPADLPIDPNEPTYCLCNQV
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                                                                 2 (bases 1 to 2817)
Zeremski,M., Hill,J., Garkavtsev,I.V. and Diatchenko,L.
Direct Submission
Submitted (16-7403-1999) Molecular Genetics, Univ. of Illinois at
Chicago, 900 South Ashland Ave., Chicago, IL 60607, USA
transcripts encode two phd finger proteins that have opposite effects on p53 function J. Biol. Chem. 274 (45), 32172-32181 (1999)
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/db_xref="taxon:10090"
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/gene="Ing1"
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